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(54) **Signal recognition particle polypeptides and polynucleotides**

(57) The invention provides histidine kinase polypeptides and DNA (RNA) encoding histidine kinase polypeptides and methods for producing such polypep-

tides by recombinant techniques. Also provided are methods for utilizing histidine kinase polypeptides to screen for antibacterial compounds.

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Description

FIELD OF THE INVENTION

5 [0001] This invention relates to newly identified polynucleotides and polypeptides, and their production and uses, as well as their variants, agonists and antagonists, and their uses. In particular, in these and in other regards, the invention relates to novel polynucleotides and polypeptides of the histidine kinase family, hereinafter referred to as "histidine kinase".

10 BACKGROUND OF THE INVENTION

[0002] The Streptococci make up a medically important genera of microbes known to cause several types of disease in humans, including, for example, otitis media, conjunctivitis, pneumonia, bacteremia, meningitis, sinusitis, pleural empyema and endocarditis, and most particularly meningitis, such as for example infection of cerebrospinal fluid. Since 15 its isolation more than 100 years ago, *Streptococcus pneumoniae* has been one of the more intensively studied microbes. For example, much of our early understanding that DNA is, in fact, the genetic material was predicated on the work of Griffith and of Avery, Macleod and McCarty using this microbe. Despite the vast amount of research with *Streptococcus pneumoniae*, many questions concerning the virulence of this microbe remain. It is particularly preferred to employ Streptococcal genes and gene products as targets for the development of antibiotics.

20 [0003] The frequency of *Streptococcus pneumoniae* infections has risen dramatically in the past 20 years. This has been attributed to the emergence of multiply antibiotic resistant strains and an increasing population of people with weakened immune systems. It is no longer uncommon to isolate *Streptococcus pneumoniae* strains which are resistant to some or all of the standard antibiotics. This has created a demand for both new anti-microbial agents and diagnostic tests for this organism.

25 [0004] While certain Streptococcal factors associated with pathogenicity have been identified, e.g., capsule polysaccharides, peptidoglycans, pneumolysins, PspA Complement factor H binding component, autolysin, neuraminidase, peptide permeases, hydrogen peroxide, IgA1 protease, the list is certainly not complete. Further very little is known concerning the temporal expression of such genes during infection and disease progression in a mammalian host. Discovering the sets of genes the bacterium is likely to be expressing at the different stages of infection, particularly 30 when an infection is established, provides critical information for the screening and characterization of novel antibacterials which can interrupt pathogenesis. In addition to providing a fuller understanding of known proteins, such an approach will identify previously unrecognized targets.

[0005] Many two component signal transduction systems (TCSTS) have been identified in bacteria (Stock, J. B., Ninfa, A.J. & Stock, A.M.(1989) Microbiol. Rev. 53, 450-490). These are involved in the bacterium's ability to monitor 35 its surroundings and adapt to changes in its environment. Several of these bacterial TCSTS are involved in virulence and bacterial pathogenesis within the host.

[0006] Histidine kinases are components of the TCSTS which autophosphorylate a histidine residue. The phosphate group is then transferred to the cognate response regulator. The histidine kinases have five short conserved amino acid sequences (Stock, J. B., Ninfa, A.J. & Stock, A.M.(1989) Microbiol. Rev. 53, 450-490, Swanson, R.V., Alex, L.A. & 40 Simon, M.I.(1994) TIBS 19 485-491). These are the histidine residue, which is phosphorylated, followed after approximately 100 residues by a conserved asparagine residue. After another 15 to 45 residues a DXGXXG motif is found, followed by a FXXF motif after another 10-20 residues. 10-20 residues further on another glycine motif, GXG is found. The two glycine motifs are thought to be involved in nucleotide binding. This family of histidine kinases includes LytS protein from *Bacillus subtilis*. LytS is the autolysin histidine kinase of the Lyt TCSTS.

45 [0007] Response regulators are components of the TCSTS. These proteins are phosphorylated by histidine kinases and in turn once phosphorylated effect the response, often through a DNA binding domain becoming activated. The response regulators are characterized by a conserved N-terminal domain of approximately 100 amino acids. The N-terminal domains of response regulators as well as retaining five functionally important residues, corresponding to the residues D12, D13, D57, T87, K109 in CheY (Matsumura, P., Rydel, J.J., Linzmeier, R. & Vacante, D. (1984) J. Bacteriol. 160, 36-41), have conserved structural features (Volz, K. (1993) Biochemistry 32, 11741-11753). The 3-dimensional 50 structures of CheY from *Salmonella typhimurium* (Stock, A.M., Mottonen, J.M., Stock, J.B. & Schutt, C.E. (1989) Nature, 337, 745-749) and *Escherichia coli* (Volz, K. & Matsumura, P. (1991) J. Biol. Chem. 266, 15511-15519) and the N-terminal domain of nitrogen regulatory protein C from *Salmonella typhimurium* (Volkman, B.F., Nohaile, M.J., Amy, N.K., Kustu, S. & Wemmer, D.E. (1995) Biochemistry, 34 1413-1424), are available, as well as the secondary structure 55 of SpoOF from *Bacillus subtilis* (Fehr, V.A., Zapf, J.W., Hoch, J.A., Dahlquist, F.W., Whiteley, J.M. & Cavanagh, J. (1995) Protein Science, 4, 1801-1814). These structures have an (a/b)⁵ fold. Several structural residues are conserved between different response regulator sequences, specifically hydrophobic residues within the β -sheet hydrophobic core and sites from the a-helices.

[0008] Among the processes regulated by TCSTS are production of virulence factors, motility, antibiotic resistance and cell replication. Inhibitors of TCSTS proteins would prevent the bacterium from establishing and maintaining infection of the host by preventing it from producing the necessary factors for pathogenesis and thereby have utility in anti-bacterial therapy.

[0009] Clearly, there is a need for factors, such as the novel compounds of the invention, that have a present benefit of being useful to screen compounds for antibiotic activity. Such factors are also useful to determine their role in pathogenesis of infection, dysfunction and disease. There is also a need for identification and characterization of such factors and their antagonists and agonists which can play a role in preventing, ameliorating or correcting infections, dysfunctions or diseases.

[0010] The polypeptides of the invention have amino acid sequence homology to a known lytS from *Bacillus subtilis* protein (Genembl 275208).

SUMMARY OF THE INVENTION

[0011] It is an object of the invention to provide polypeptides that have been identified as novel histidine kinase polypeptides by homology between the amino acid sequence set out in Table 1 [SEQ ID NO: 2] and a known amino acid sequence or sequences of other proteins such as lytS from *Bacillus subtilis* protein (Genembl 275208).

[0012] It is a further object of the invention to provide polynucleotides that encode histidine kinase polypeptides, particularly polynucleotides that encode the polypeptide herein designated histidine kinase.

[0013] In a particularly preferred embodiment of the invention, the polynucleotide comprises a region encoding histidine kinase polypeptides comprising the sequence set out in Table 1 [SEQ ID NO:1] which includes a full length gene, or a variant thereof.

[0014] In another particularly preferred embodiment of the invention, there is a novel histidine kinase protein from *Streptococcus pneumoniae* comprising the amino acid sequence of Table 1 [SEQ ID NO:2], or a variant thereof.

[0015] In accordance with another aspect of the invention, there is provided an isolated nucleic acid molecule encoding a mature polypeptide expressible by the *Streptococcus pneumoniae* 0100993 strain contained in the deposited strain.

[0016] As a further aspect of the invention, there are provided isolated nucleic acid molecules encoding histidine kinase, particularly *Streptococcus pneumoniae* histidine kinase, including mRNAs, cDNAs, genomic DNAs. Further embodiments of the invention include biologically, diagnostically, prophylactically, clinically or therapeutically useful variants thereof, and compositions comprising the same.

[0017] In accordance with another aspect of the invention, there is provided the use of a polynucleotide of the invention for therapeutic or prophylactic purposes, in particular genetic immunization. Among the particularly preferred embodiments of the invention are naturally occurring allelic variants of histidine kinase and polypeptides encoded thereby.

[0018] As another aspect of the invention, there are provided novel polypeptides of *Streptococcus pneumoniae* referred to herein as histidine kinase as well as biologically, diagnostically, prophylactically, clinically or therapeutically useful variants thereof, and compositions comprising the same.

[0019] Among the particularly preferred embodiments of the invention are variants of histidine kinase polypeptide encoded by naturally occurring alleles of the histidine kinase gene.

[0020] In a preferred embodiment of the invention, there are provided methods for producing the aforementioned histidine kinase polypeptides.

[0021] In accordance with yet another aspect of the invention, there are provided inhibitors to such polypeptides, useful as antibacterial agents, including, for example, antibodies.

[0022] In accordance with certain preferred embodiments of the invention, there are provided products, compositions and methods for assessing histidine kinase expression, treating disease, for example, otitis media, conjunctivitis, pneumonia, bacteremia, meningitis, sinusitis, pleural empyema and endocarditis, and most particularly meningitis, such as for example infection of cerebrospinal fluid, assaying genetic variation, and administering a histidine kinase polypeptide or polynucleotide to an organism to raise an immunological response against a bacteria, especially a *Streptococcus pneumoniae* bacteria.

[0023] In accordance with certain preferred embodiments of this and other aspects of the invention, there are provided polynucleotides that hybridize to histidine kinase polynucleotide sequences, particularly under stringent conditions.

[0024] In certain preferred embodiments of the invention, there are provided antibodies against histidine kinase polypeptides.

[0025] In other embodiments of the invention, there are provided methods for identifying compounds which bind to or otherwise interact with and inhibit or activate an activity of a polypeptide or polynucleotide of the invention comprising: contacting a polypeptide or polynucleotide of the invention with a compound to be screened under conditions to permit binding to or other interaction between the compound and the polypeptide or polynucleotide to assess the binding to

or other interaction with the compound, such binding or interaction being associated with a second component capable of providing a detectable signal in response to the binding or interaction of the polypeptide or polynucleotide with the compound; and determining whether the compound binds to or otherwise interacts with and activates or inhibits an activity of the polypeptide or polynucleotide by detecting the presence or absence of a signal generated from the binding or interaction of the compound with the polypeptide or polynucleotide.

[0026] In accordance with yet another aspect of the invention, there are provided histidine kinase agonists and antagonists, preferably bacteriostatic or bacteriocidal agonists and antagonists.

[0027] In a further aspect of the invention, there are provided compositions comprising a histidine kinase polynucleotide or a histidine kinase polypeptide for administration to a cell or to a multicellular organism.

[0028] Various changes and modifications within the spirit and scope of the disclosed invention will become readily apparent to those skilled in the art from reading the following descriptions and from reading the other parts of the present disclosure.

GLOSSARY

[0029] The following definitions are provided to facilitate understanding of certain terms used frequently herein.

[0030] "Host cell" is a cell which has been transformed or transfected, or is capable of transformation or transfection by an exogenous polynucleotide sequence.

[0031] "Identity," as known in the art, is a relationship between two or more polypeptide sequences or two or more polynucleotide sequences, as determined by comparing the sequences. In the art, "identity" also means the degree of sequence relatedness between polypeptide or polynucleotide sequences, as the case may be, as determined by the match between strings of such sequences. "Identity" and "similarity" can be readily calculated by known methods, including but not limited to those described in (*Computational Molecular Biology*, Lesk, A.M., ed., Oxford University Press, New York, 1988; *Biocomputing: Informatics and Genome Projects*, Smith, D.W., ed., Academic Press, New York, 1993; *Computer Analysis of Sequence Data*, Part I, Griffin, A.M., and Griffin, H.G., eds., Humana Press, New Jersey, 1994; *Sequence Analysis in Molecular Biology*, von Heinje, G., Academic Press, 1987; and *Sequence Analysis Primer*, Gribskov, M. and Devereux, J., eds., M Stockton Press, New York, 1991; and Carillo, H., and Lipman, D., *SIAM J. Applied Math.*, 48: 1073 (1988). Preferred methods to determine identity are designed to give the largest match between the sequences tested. Methods to determine identity and similarity are codified in publicly available computer programs. Preferred computer program methods to determine identity and similarity between two sequences include, but are not limited to, the GCG program package (Devereux, J., et al., *Nucleic Acids Research* 12(1): 387 (1984)), BLASTP, BLASTN, and FASTA (Altschul, S.F. et al., *J. Molec. Biol.* 215: 403-410 (1990)). The BLAST X program is publicly available from NCBI and other sources (*BLAST Manual*, Altschul, S., et al., NCBI NLM NIH Bethesda, MD 20894; Altschul, S., et al., *J. Mol. Biol.* 215: 403-410 (1990)). As an illustration, by a polynucleotide having a nucleotide sequence having at least, for example, 95% "identity" to a reference nucleotide sequence of SEQ ID NO: 1 it is intended that the nucleotide sequence of the polynucleotide is identical to the reference sequence except that the polynucleotide sequence may include up to five point mutations per each 100 nucleotides of the reference nucleotide sequence of SEQ ID NO: 1. In other words, to obtain a polynucleotide having a nucleotide sequence at least 95% identical to a reference nucleotide sequence, up to 5% of the nucleotides in the reference sequence may be deleted or substituted with another nucleotide, or a number of nucleotides up to 5% of the total nucleotides in the reference sequence may be inserted into the reference sequence. These mutations of the reference sequence may occur at the 5' or 3' terminal positions of the reference nucleotide sequence or anywhere between those terminal positions, interspersed either individually among nucleotides in the reference sequence or in one or more contiguous groups within the reference sequence. Analogously, by a polypeptide having an amino acid sequence having at least, for example, 95% identity to a reference amino acid sequence of SEQ ID NO: 2 is intended that the amino acid sequence of the polypeptide is identical to the reference sequence except that the polypeptide sequence may include up to five amino acid alterations per each 100 amino acids of the reference amino acid of SEQ ID NO: 2. In other words, to obtain a polypeptide having an amino acid sequence at least 95% identical to a reference amino acid sequence, up to 5% of the amino acid residues in the reference sequence may be deleted or substituted with another amino acid, or a number of amino acids up to 5% of the total amino acid residues in the reference sequence may be inserted into the reference sequence. These alterations of the reference sequence may occur at the amino or carboxy terminal positions of the reference amino acid sequence or anywhere between those terminal positions, interspersed either individually among residues in the reference sequence or in one or more contiguous groups within the reference sequence.

[0032] "Isolated" means altered "by the hand of man" from its natural state, i.e., if it occurs in nature, it has been changed or removed from its original environment, or both. For example, a polynucleotide or a polypeptide naturally present in a living organism is not "isolated," but the same polynucleotide or polypeptide separated from the coexisting materials of its natural state is "isolated", as the term is employed herein.

[0033] "Polynucleotide(s)" generally refers to any polyribonucleotide or polynucleotide, which may be un-

modified RNA or DNA or modified RNA or DNA. "Polynucleotide(s)" include, without limitation, single- and double-stranded DNA, DNA that is a mixture of single- and double-stranded regions or single-, double- and triple-stranded regions, single- and double-stranded RNA, and RNA that is mixture of single- and double-stranded regions, hybrid molecules comprising DNA and RNA that may be single-stranded or, more typically, double-stranded, or triple-stranded regions, or a mixture of single- and double-stranded regions. In addition, "polynucleotide" as used herein refers to triple-stranded regions comprising RNA or DNA or both RNA and DNA. The strands in such regions may be from the same molecule or from different molecules. The regions may include all of one or more of the molecules, but more typically involve only a region of some of the molecules. One of the molecules of a triple-helical region often is an oligonucleotide. As used herein, the term "polynucleotide(s)" also includes DNAs or RNAs as described above that contain one or more modified bases. Thus, DNAs or RNAs with backbones modified for stability or for other reasons are "polynucleotide(s)" as that term is intended herein. Moreover, DNAs or RNAs comprising unusual bases, such as inosine, or modified bases, such as tritylated bases, to name just two examples, are polynucleotides as the term is used herein. It will be appreciated that a great variety of modifications have been made to DNA and RNA that serve many useful purposes known to those of skill in the art. The term "polynucleotide(s)" as it is employed herein embraces such chemically, enzymatically or metabolically modified forms of polynucleotides, as well as the chemical forms of DNA and RNA characteristic of viruses and cells, including, for example, simple and complex cells. "Polynucleotide(s)" also embraces short polynucleotides often referred to as oligonucleotide(s).

[0034] "Polypeptide(s)" refers to any peptide or protein comprising two or more amino acids joined to each other by peptide bonds or modified peptide bonds. "Polypeptide(s)" refers to both short chains, commonly referred to as peptides, oligopeptides and oligomers and to longer chains generally referred to as proteins. Polypeptides may contain amino acids other than the 20 gene encoded amino acids. "Polypeptide(s)" include those modified either by natural processes, such as processing and other post-translational modifications, but also by chemical modification techniques. Such modifications are well described in basic texts and in more detailed monographs, as well as in a voluminous research literature, and they are well known to those of skill in the art. It will be appreciated that the same type of modification may be present in the same or varying degree at several sites in a given polypeptide. Also, a given polypeptide may contain many types of modifications. Modifications can occur anywhere in a polypeptide, including the peptide backbone, the amino acid side-chains, and the amino or carboxyl termini. Modifications include, for example, acetylation, acylation, ADP-ribosylation, amidation, covalent attachment of flavin, covalent attachment of a heme moiety, covalent attachment of a nucleotide or nucleotide derivative, covalent attachment of a lipid or lipid derivative, covalent attachment of phosphatidylinositol, cross-linking, cyclization, disulfide bond formation, demethylation, formation of covalent cross-links, formation of cysteine, formation of pyroglutamate, formylation, gamma-carboxylation, glycosylation, GPI anchor formation, hydroxylation, iodination, methylation, myristoylation, oxidation, proteolytic processing, phosphorylation, prenylation, racemization, glycosylation, lipid attachment, sulfation, gamma-carboxylation of glutamic acid residues, hydroxylation and ADP-ribosylation, selenoylation, sulfation, transfer-RNA mediated addition of amino acids to proteins, such as arginylation, and ubiquitination. See, for instance, *PROTEINS - STRUCTURE AND MOLECULAR PROPERTIES*, 2nd Ed., T. E. Creighton, W. H. Freeman and Company, New York (1993) and Wold, F., Posttranslational Protein Modifications: Perspectives and Prospects, pgs. 1-12 in *POSTTRANSLATIONAL COVALENT MODIFICATION OF PROTEINS*, B. C. Johnson, Ed., Academic Press, New York (1983); Seifter et al., *Meth. Enzymol.* 182:626-646 (1990) and Rattan et al., *Protein Synthesis: Posttranslational Modifications and Aging*, Ann. N.Y. Acad. Sci. 663: 48-62 (1992). Polypeptides may be branched or cyclic, with or without branching. Cyclic, branched and branched circular polypeptides may result from post-translational natural processes and may be made by entirely synthetic methods, as well.

[0035] "Variant(s)" as the term is used herein, is a polynucleotide or polypeptide that differs from a reference polynucleotide or polypeptide respectively, but retains essential properties. A typical variant of a polynucleotide differs in nucleotide sequence from another, reference polynucleotide. Changes in the nucleotide sequence of the variant may or may not alter the amino acid sequence of a polypeptide encoded by the reference polynucleotide. Nucleotide changes may result in amino acid substitutions, additions, deletions, fusions and truncations in the polypeptide encoded by the reference sequence, as discussed below. A typical variant of a polypeptide differs in amino acid sequence from another, reference polypeptide. Generally, differences are limited so that the sequences of the reference polypeptide and the variant are closely similar overall and, in many regions, identical. A variant and reference polypeptide may differ in amino acid sequence by one or more substitutions, additions, deletions in any combination. A substituted or inserted amino acid residue may or may not be one encoded by the genetic code. A variant of a polynucleotide or polypeptide may be a naturally occurring such as an allelic variant, or it may be a variant that is not known to occur naturally. Non-naturally occurring variants of polynucleotides and polypeptides may be made by mutagenesis techniques, by direct synthesis, and by other recombinant methods known to skilled artisans.

DESCRIPTION OF THE INVENTION

[0036] The invention relates to novel histidine kinase polypeptides and polynucleotides as described in greater detail below. In particular, the invention relates to polypeptides and polynucleotides of a novel histidine kinase of *Streptococcus pneumoniae*, which is related by amino acid sequence homology to lytS from *Bacillus subtilis* polypeptide. The invention relates especially to a histidine kinase having the nucleotide and amino acid sequences set out in Table 1 [SEQ ID NO: 1] and Table 1 [SEQ ID NO: 2] respectively, and to the histidine kinase nucleotide sequences of the DNA in the deposited strain and amino acid sequences encoded thereby.

TABLE 1**Histidine kinase Polynucleotide and Polypeptide Sequences**

(A) Sequences from *Streptococcus pneumoniae* histidine kinase polynucleotide sequence
[SEQ ID NO:1].

5 5'-1 CTTATATGCA GAACATGGTT ATAGCTTTCG GGAATACAGT TTGAAGGAGG

10 51 CTTGGTCTCT TTACAAGCAA AATTTTATCT CAAGCAACCT GATTTTCTAT

10 101 AGCTTTTATAG GTGTGGGTCT AGTTTGTACC TATGGTTTGT ATCTCTTGGT

15 151 GCAATTGCCT CATCAGACCA TTGTTCAATT GATTGCGACC CTTTGAATG

15 201 TCCTAGTAGT TGCCCTGATC TTTTGGCTT ATACAGTATC TTTAAAATTA

20 251 CAAGTTTATT TTGCCCTTGT CTATCGAAAT AGTCTCAAAT TATCCTTGAT

20 301 TGGCATCTTT ATGAGTCTAG CAGCTGTGGC TAAGGTTCTC CTTGGGACTG

25 351 TGCTACTTGT AGCAATTGGT TACTATATGC CTGCCCTGCT ATTTTTTGTA

25 401 GGAATTGGGA TGTGGCATT CTTTATCAGT GATATGTTGG AACCTGTCTA

30 451 TGAAATCATC CATGAAAAAT TGGCGACAAA ATAGAATGAA GCACTTTTGG

30 501 CTACATACGC TTCTAAGAAC CTATAGTTCA GTGATGATCA TTATCATTGC

35 551 GAGTTTGTCA ATCTTACTCT CTTACGCTGA CTGGGATTCA CGTGAAAAGG

35 601 AAGCCCAGAG AGTAGCCCAG CGTGTAAGT CTAGAACAGT GAGTGAAATT

40 651 GAATATTACC ATAGAGAGTC AAGCCAGATA GCTCAGGCTT TAGTTGAAAA

40 701 CCAAGCTCGT ATGAGGGAA TCTATAAATA CTTTAGCCTT AGCATGCCAG

45 751 ACTATTTTTA CTGGCAATTA GAGCGGAAAG CTTGCGCTTA TATATCAGTC

45 801 TCTCTGTATG AAAATGTTGA TGACCTCTAT GTTCGAAATG ATTTTGTAAC

50 851 TGGGGTGGCC ATTGCTTTTC AAGATTACAA GGAAGTCTAT GTTCTACTA

55

901 AAGACAAACG TAGTGGAGAA AAAATCAGGG CTGAGGATTT CAAACCAGCA
5 951 GGAAATAGTT TTGCCATTCC AGTGTGAGAT CCAGTGTGAG ATCAAGACTT
1001 AGGAGTGATT TACATCTCCT TGGATCCTGC TGTTTTATAC CATGCCATTG
10 1051 ATAATACTAG AGGTCATACT CCGATGGCAG TAACAGTGAC CGAACCTTTT
1101 GATACGGAGA TTTTTCATAT TGGTGAGACA GTTGATAAGG AGAGTGAAAA
15 1151 TTGGCTAGTT GGCTTAACTT CTCATGGTTA TCAGGTTGAG GTGGCAGTTC
1201 CCAAAAACCTT TGTTTTACAA GGAACGGTGA CCAGCTCTGC TTTGATTGTG
20 1251 GGCTTGAGCC TTCTCTTTAT TGTCATTCTT TATCTGACTT TGAGGCAGAC
1301 CTTTGCTAAT TATCAAAAGC AGGTAGTGGA TTTGGTGGAT TCCATCCAAG
25 1351 CTATTGCCCA AGGACAAGAA GGTCTTCGCA TTGATACGCT TGAAAAGGAT
1401 CAGGAATTGC TCCTAATCGC GGAGACGACC AATGATATGT TGGATCGATT
30 1451 GGAAAAGAAT ATCCATGATA TTTACCAGTT AGAACTCAGT CAAAAGATG
1501 CCAATATGCG GGCCTTGAG GCGCAAATCA ATCCTCATTT TATGTATAAT
35 1551 ACGCTGGAGT TCTTGCGCAT GTATGCAGTT ATGCAGAGTC AAGATGAGTT
1601 GGCAGATATC ATTTATGAAT TCAGTAGTCT CTTGCGTAAC AATATTTCCG
40 1651 ACGAAAGAGA GACCCTCCTC AAACAGGAAT TAGAATTTTG CCGTAAATAC
1701 AGCTATCTCT GCATGGTTCG CTATCCCAAG TCCATTGCCT ATGGTTTCAA
45 1751 GATAGATCCA GAGTTAGAGA ATATGAAGAT TCCCAAGTTT ACCTTGCAAC
50 1801 CGCTGGTAGA AACTATTTT CCGCATGGTG TTGACCACAG GCGGACAGAT
1851 AATGTGATTA GCATCAAGGC TCTTAAACAG GATGGTTTTG TGAAATTTT
55

5

1901 GGTGGTCGAT AATGGTAGAG GAATGTCGGC TGAAAAGTTG GCAAATATCC

1951 GAGAAAAATT AAGTCAGAGA TATTTTGAAC ACCAAGCCAG CTACAGTGAT

10

2001 CAAAGGCAGT CTATCGGGAT TGTCAATGTA CACGAGCGTT TTGTGCTCTA

2051 TTTTGGAGAC CGCTATGCCA TTA CTATAGA GTCTGCAGAG CAAGCCGGTG

15

2101 TTCAGTATCG TATTACAATT CAAGATGAGT AGAAAGGGAG AAAATGTATA

2151 AAGTATTATT AGTAGATGAT GAGTACATGG TGACAGAAGG TCTGAAGCGT

20

2201 TTGATTCCCT TTGATAAGTG GGATATGGAG GTCGTCGCAA CAGTCAGTCA

2251 TGCCGATGAA GCTCTAGAAT ATGTT CAGGA AAATCCTGTC GATGTCATCA

25

2301 TTTCCGATGT CAATATGCCA GACAAAACAG GGCTTGATAT GATTCCGGGAG

2351 ATGAAAGAGA TCTTACCAGA TGCTGCCTAT ATCCTGCTCT CAGGTTATCA

30

2401 GGAGTTTGAT TATGTAAAAA GAGCAATGAA TCTTAGTGTG GTGGACTATT

2451 TGGTCAAACC TGTTGATAAG GTAGAGCTGG GAAATCTGCT GGAGAAGATT

35

2501 GCAGGTCAGC TCGGCGAGAG AGGGAAGAAA AGTCAGACTC TTAGTCAAGA

2551 ATTAGACGAG GCTGGATTTG TTAGTTATTT AGGGGATAAG GAGAATTGGT

40

2601 GGATAGGTCT ATCCAAGGAA AAACAAGGTT CCTTCACCAT TCCCTACTAT

2651 GTCTTGGGTC AAGCCTGGCA GATTTTCATT TCTGACCAAC CCCTAGATGG

45

2701 TTTAGTCGTT ACACCTTTTG AAGCTCCTTA TCAAGAACAT TTTGAACGCT

2751 GGAAGCTGAA TGCTGAGAAA ACCCTCTTTT ACGGTTCTGT AAATCTGCAG

50

2801 CAGTCTGAGA GTCTCTTTGC CTATTACGAA CCGATTTATA GGGTTATCAT

55

2851 TCAGGGAAAT CTCAATCAAA TCGTAGAAGA GTTAAATCTC TTGGAGAAGG
5 2901 TAGTTCTTGA AAATACGCCG CGAATTCCGA TTACTAAACA GCTTTTTATC
2951 CAGTTTGTCA TGGATGTCTT CCATTTATTT GAACATCTCA AAGCTGATGA
10 3001 TATGACGGAC ATTGTCAAAA CCATTCATGC TATTCAATCC TTCGATGAAT
3051 TGGTTTCTTA TATCAAGGAA ACTCTGATCA GCTTTTTTCGG TCAATACCGT
15 3101 ATGAATGAAA ATGTGGTCAG TGTGCTGGAA GTCATTGGTC GTGATTACCA
3151 AAAAGAGCTT TCCCTCAAGG ATATCAGTAA GGCCCTCTTT ATCAATCCTG
20 3201 TCTATCTAGG GCAGTTGATT AAGCGTGAAA CCGATTGAC CTTTGCAGAG
3251 TTACTAAACA AACAACGTAT TAAGGCTGCC CAACAACTTT TGCTTTCAAC
25 3301 TAGTGACAGC ATCGAAAATA TTTGTTATGC TGTTGGTTAC AGTAACCTTG
3351 GATATTTCTA TAAAGTTTTT CGAAAATTGT GCGGAAAATC GCCAAAAGCC
30 3401 TACCGAAAAC AGGTAGAAAC TATACTATAA GATTGTATT CCTTTACAAA
3451 ATG-3'
35
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45
50
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(B) Histidine kinase polypeptide sequence deduced from the polynucleotide sequence in this table [SEQ ID NO:2].

5 NH₂-1 MKSSMKNWRQ NRMKHFVLT LLRTYSSVMI IIIASFALL SYADWDSREK

10 51 EAQRVAQRVT ARTVSEIEYY HRESTQIAQA LVENQARIEG IYKYFSLSMP

101 DYFYWQLERK ASPYISVSLY ENVDDLYVRN DFVTGVAF QDYKEVYST

15 151 KDKRSGEKIR AEDFKPAGNS FAIPVSDPVS DQDLGVIIYS LDPVLYHAI

201 DNTRGHTPMA VTVTEPFDTE IFHIGETVDK ESENWLVLGT SHGYQVQVAV

25 251 PKNFVLQGTV TSSALIVGLS LLFIVILYLT LRQTFANYQK QVVDLVDSIQ

301 AIAQQQEGLR IDTLEKDQEL LLIAETNDM LDRLEKNIHD IYQLELSQKD

35 351 ANMRALQAQI NPHFMYNTLE FLRMVAVMQS QDELADIIYE FSSLLRNNIS

401 DERETLLKQE LEFCRKYSYL CMVRYPKSIA YGFKIDPELE NMKIPKFTLQ

45 451 PLVENYFAHG VDHRRTDNVI SIKALKQDGF VEILVVDNGR GMSAEKLANI

501 REKLSQRYFE HQASYSDQRQ SIGIVNVHER FVLYFGDRYA ITIESAEQAG

55 551 VQYRITIQDE-COOH

(C) Polynucleotide sequence embodiments [SEQ ID NO:1].

40 X-(R₁)_n-1 CTTATATGCA GAACATGGTT ATAGCTTTCG GGAATACAGT TTGAAGGAGG

51 CTTGGTCTCT TTACAAGCAA AATTTTATCT CAAGCAACCT GATTTTCTAT

45 101 AGCTTTTATG GTGTGGGTCT AGTTTGTACC TATGGTTTGT ATCTCTTGGT

151 GCAATTGCCT CATCAGACCA TTGTTCAATTT GATTGCGACC CTTTGAATG

50 201 TCCTAGTAGT TGCCCTGATC TTTTGGCTT ATACAGTATC TTTAAATTA

251 CAAGTTTATT TTGCCTTGTC CTATCGAAAT AGTCTCAAAT TATCCTTGAT

55

301 TGGCATCTTT ATGAGTCTAG CAGCTGTGGC TAAGGTTCTC CTTGGGACTG
5
351 TGCTACTTGT AGCAATTGGT TACTATATGC CTGCCCTGCT ATTTTTTGTA
10
401 GGAATTGGGA TGTGGCATT CTTTATCAGT GATATGTTGG AACCTGTCTA
15
451 TGAAATCATC CATGAAAAAT TGGCGACAAA ATAGAATGAA GCACTTTTGG
501 CTACATACGC TTCTAAGAAC CTATAGTTCA GTGATGATCA TTATCATTGC
20
551 GAGTTTTGCA ATCTTACTCT CTTACGCTGA CTGGGATTCA CGTGAAAAGG
601 AAGCCCAGAG AGTAGCCCAG CGTGTAAGT CTAGAACAGT GAGTGAAATT
25
651 GAATATTACC ATAGAGAGTC AACCCAGATA GCTCAGGCTT TAGTTGAAAA
701 CCAAGCTCGT ATTGAGGGAA TCTATAAATA CTTTAGCCTT AGCATGCCAG
30
751 ACTATTTTTA CTGGCAATTA GAGCGGAAAG CTTGCCTTA TATATCAGTC
801 TCTCTGTATG AAAATGTTGA TGACCTCTAT GTTCGAAATG ATTTTGTAAC
35
851 TGGGGTGGCC ATTGCTTTTC AAGATTACAA GGAAGTCTAT GTTTCTACTA
901 AAGACAAACG TAGTGGAGAA AAAATCAGGG CTGAGGATTT CAAACCAGCA
40
951 GGAAATAGTT TTGCCATTCC AGTGTGAGAT CCAGTGTGAG ATCAAGACTT
1001 AGGAGTGATT TACATCTCCT TGGATCCTGC TGTTTTATAC CATGCCATTG
45
1051 ATAATACTAG AGGTCATACT CCGATGGCAG TAACAGTGAC CGAACCTTTT
1101 GATACGGAGA TTTTTCATAT TGGTGAGACA GTTGATAAGG AGAGTGAAAA
50
1151 TTGGCTAGTT GGCTTAACTT CTCATGGTTA TCAGGTTTCA GTGGCAGTTC
1201 CCAAAAACCTT TGTTTTACAA GGAACGGTGA CCAGCTCTGC TTTGATTGTG
55

1251 GGCTTGAGCC TTCTCTTTAT TGTCAATTCTT TATCTGACTT TGAGGCAGAC
5 1301 CTTTGCTAAT TATCAAAAGC AGGTAGTGGA TTTGGTGGAT TCCATCCAAG
1351 CTATTGCCCCA AGGACAAGAA GGTCTTCGCA TTGATACGCT TGAAAAGGAT
10 1401 CAGGAATTGC TCCTAATCGC GGAGACGACC AATGATATGT TGGATCGATT
1451 GGAAAAGAAT ATCCATGATA TTTACCAGTT AGAACTCAGT CAAAAAGATG
15 1501 CCAATATGCG GGCCTTGCG GCGCAAATCA ATCCTCATTT TATGTATAAT
1551 ACGCTGGAGT TCTTGCGCAT GTATGCAGTT ATGCAGAGTC AAGATGAGTT
20 1601 GGCAGATATC ATTTATGAAT TCAGTAGTCT CTTGCGTAAC AATATTTCCG
1651 ACGAAAGAGA GACCCTCCTC AAACAGGAAT TAGAATTTTG CCGTAAATAC
25 1701 AGCTATCTCT GCATGGTTCG CTATCCCAAG TCCATTGCCT ATGGTTTCAA
1751 GATAGATCCA GAGTTAGAGA ATATGAAGAT TCCCAAGTTT ACCTTGCAAC
30 1801 CGCTGGTAGA AAACATTTTC GCGCATGGTG TTGACCACAG GCGGACAGAT
1851 AATGTGATTA GCATCAAGGC TCTTAAACAG GATGGTTTTG TGGAAATTTT
35 1901 GGTGGTCGAT AATGGTAGAG GAATGTCGGC TGAAAAGTTG GCAAATATCC
1951 GAGAAAAATT AAGTCAGAGA TATTTTGAAC ACCAAGCCAG CTACAGTGAT
40 2001 CAAAGGCAGT CTATCGGGAT TGTCAATGTA CACGAGCGTT TTGTGCTCTA
2051 TTTTGGAGAC CGCTATGCCA TTAATATAGA GTCTGCAGAG CAAGCCGGTG
45 2101 TTCAGTATCG TATTACAATT CAAGATGAGT AGAAAGGGAG AAAATGTATA
2151 AAGTATTATT AGTAGATGAT GAGTACATGG TGACAGAAGG TCTGAAGCGT
50 2201 TTGATTCCCT TTGATAAGTG GGATATGGAG GTCGTCGCAA CAGTCAGTCA
55

5

2251 TGCCGATGAA GCTCTAGAAT ATG TTCAGGA AAATCCTGTC GATGTCATCA

2301 TTTCCGATGT CAATATGCCA GACAAAACAG GGCTTGATAT GATTCGGGAG

10

2351 ATGAAAGAGA TCTTACCAGA TGCTGCCTAT ATCCTGCTCT CAGGTTATCA

2401 GGAGTTTGAT TATGTAAAAA GAGCAATGAA TCTTAGTGTG GTGGACTATT

15

2451 TGGTCAAACC TGTTGATAAG GTAGAGCTGG GAAATCTGCT GGAGAAGATT

2501 GCAGGTCAGC TCGGCGAGAG AGGGAAGAAA AGTCAGACTC TTAGTCAAGA

20

2551 ATTAGACGAG GCTGGATTTG TTAGTTATTT AGGGGATAAG GAGAATTGGT

2601 GGATAGGTCT ATCCAAGGAA AAACAAGGTT CCTTCACCAT TCCCTACTAT

25

2651 GTCTTGCGTC AAGCCTGGCA GATTTTCATT TCTGACCAAC CCCTAGATGG

2701 TTTAGTCGTT ACACCTTTTG AAGCTCCTTA TCAAGAACAT TTTGAACGCT

30

2751 GGAAGCTGAA TGCTGAGAAA ACCCTCTTTT ACGGTTCTGT AAATCTGCAG

2801 CAGTCTGAGA GTCTCTTTGC CTATTACGAA CCGATTTATA GGGTTATCAT

35

2851 TCAGGGAAAT CTCAATCAAA TCGTAGAAGA GTTAAATCTC TTGGAGAAGG

2901 TAGTTCTTGA AAATACGCCG CGAATTCCGA TTAATAACA GCTTTTTATC

40

2951 CAGTTTGTCA TGGATGTCTT CCATTTATTT GAACATCTCA AAGCTGATGA

3001 TATGACGGAC ATTGTCAAAA CCATTCATGC TATTCAATCC TTCGATGAAT

45

3051 TGGTTTCTTA TATCAAGGAA ACTCTGATCA GCTTTTTCGG TCAATACCGT

3101 ATGAATGAAA ATGTGGTCAG TGTGCTGGAA GTCATTGGTC GTGATTACCA

50

3151 AAAAGAGCTT TCCCTCAAGG ATATCAGTAA GGCCCTCTTT ATCAATCCTG

55

3201 TCTATCTAGG GCAGTTGATT AAGCGTGAAA CCGATTCGAC CTTTGCAGAG
 5 3251 TTACTAAACA AACAACTAT TAAGGCTGCC CAACAACTTT TGCTTTCAAC
 3301 TAGTGACAGC ATCGAAAATA TTTGTTATGC TGTGTTAC AGTAACCTTG
 10 3351 GATATTTCTA TAAAGTTTTC CGAAAATTGT GCGGAAAATC GCCAAAAGCC
 3401 TACCGAAAAC AGGTAGAAAC TATACTATAA GATTTGTATT CCTTTACAA
 15 3451 ATG- (R₂)_n-Y

(D) Polypeptide sequence embodiments [SEQ ID NO:2].

20 X-(R₁)_n-1 MKSSMKNWRQ NRMKHFWLHT LLRTYSSVMI IIIASFALL SYADWDSREK
 51 EAQRVAQRVT ARTVSEIEYY HRESTQIAQA LVENQARIEG IYKYFSLSMP
 25 101 DYFYWQLERK ASPYISVSLY ENVDDLVRN DFVTGVAIAF QDYKEVYVST
 151 KDKRSGEKIR AEDFKPAGNS FAIPVSDPVS DQDLGVIYIS LDPVLYHAI
 30 201 DNTRGHTPMA VTVTEPFDTE IFHIGETVDK ESENWLVLGT SHGYQVQVAV
 251 PKNFVLQGTV TSSALIVGLS LLFIVILYLT LRQTFANYQK QVVDLVDSIQ
 35 301 AIAQGQEGLR IDTLEKDQEL LLIAETTNDM LDRLEKNIHD IYQLELSQKD
 351 ANMRALQAQI NPHFMYNTLE FLRMVAVMQS QDELADIYE FSSLLRNNIS
 40 401 DERETLLKQE LEFCRKYSYL CMVRYPKSIA YGFKIDPELE NMKIPKFTLQ
 451 PLVENYFAHG VDHRRTDNVI SIKALKQDGF VEILVVDNGR GMSAEKLANI
 45 501 REKLSQRYFE HQASYSDQRQ SIGIVNVHER FVLYFGDRYA ITIESAEQAG
 50 551 VQYRITIQDE-(R₂)_n-Y

Deposited materials

55 [0037] A deposit containing a *Streptococcus pneumoniae* 0100993 strain has been deposited with the National Collections of Industrial and Marine Bacteria Ltd. (herein "NCIMB"), 23 St. Machar Drive, Aberdeen AB2 1FY, Scotland on 11 April 1996 and assigned deposit number 40794. The deposit was described as *Streptococcus pneumoniae* 0100993 on deposit. On 17 April 1996 a *Streptococcus pneumoniae* 0100993 DNA library in *E. coli* was similarly deposited with

the NCIMB and assigned deposit number 40800. The *Streptococcus pneumoniae* strain deposit is referred to herein as "the deposited strain" or as "the DNA of the deposited strain."

[0038] The deposited strain contains the full length histidine kinase gene. The sequence of the polynucleotides contained in the deposited strain, as well as the amino acid sequence of the polypeptide encoded thereby, are controlling in the event of any conflict with any description of sequences herein.

[0039] The deposit of the deposited strain has been made under the terms of the Budapest Treaty on the International Recognition of the Deposit of Micro-organisms for Purposes of Patent Procedure. The strain will be irrevocably and without restriction or condition released to the public upon the issuance of a patent. The deposited strain is provided merely as convenience to those of skill in the art and is not an admission that a deposit is required for enablement, such as that required under 35 U.S.C. §112.

[0040] A license may be required to make, use or sell the deposited strain, and compounds derived therefrom, and no such license is hereby granted.

Polypeptides

[0041] The polypeptides of the invention include the polypeptide of Table 1 [SEQ ID NO:2] (in particular the mature polypeptide) as well as polypeptides and fragments, particularly those which have the biological activity of histidine kinase, and also those which have at least 70% identity to the polypeptide of Table 1 [SEQ ID NO:2] or the relevant portion, preferably at least 80% identity to the polypeptide of Table 1 [SEQ ID NO:2], and more preferably at least 90% similarity (more preferably at least 90% identity) to the polypeptide of Table 1 [SEQ ID NO:2] and still more preferably at least 95% similarity (still more preferably at least 95% identity) to the polypeptide of Table 1 [SEQ ID NO:2] and also include portions of such polypeptides with such portion of the polypeptide generally containing at least 30 amino acids and more preferably at least 50 amino acids.

[0042] The invention also includes polypeptides of the formula set forth in Table 1 (D) wherein, at the amino terminus, X is hydrogen, and at the carboxyl terminus, Y is hydrogen or a metal, R_1 and R_2 is any amino acid residue, and n is an integer between 1 and 1000. Any stretch of amino acid residues denoted by either R group, where R is greater than 1, may be either a heteropolymer or a homopolymer, preferably a heteropolymer.

[0043] A fragment is a variant polypeptide having an amino acid sequence that entirely is the same as part but not all of the amino acid sequence of the aforementioned polypeptides. As with histidine kinase polypeptides fragments may be "free-standing," or comprised within a larger polypeptide of which they form a part or region, most preferably as a single continuous region, a single larger polypeptide.

[0044] Preferred fragments include, for example, truncation polypeptides having a portion of the amino acid sequence of Table 1 [SEQ ID NO:2], or of variants thereof, such as a continuous series of residues that includes the amino terminus, or a continuous series of residues that includes the carboxyl terminus. Degradation forms of the polypeptides of the invention in a host cell, particularly a *Streptococcus pneumoniae*, are also preferred. Further preferred are fragments characterized by structural or functional attributes such as fragments that comprise alpha-helix and alpha-helix forming regions, beta-sheet and beta-sheet-forming regions, turn and turn-forming regions, coil and coil-forming regions, hydrophilic regions, hydrophobic regions, alpha amphipathic regions, beta amphipathic regions, flexible regions, surface-forming regions, substrate binding region, and high antigenic index regions.

[0045] Also preferred are biologically active fragments which are those fragments that mediate activities of histidine kinase, including those with a similar activity or an improved activity, or with a decreased undesirable activity. Also included are those fragments that are antigenic or immunogenic in an animal, especially in a human. Particularly preferred are fragments comprising receptors or domains of enzymes that confer a function essential for viability of *Streptococcus pneumoniae* or the ability to initiate, or maintain cause disease in an individual, particularly a human.

[0046] Variants that are fragments of the polypeptides of the invention may be employed for producing the corresponding full-length polypeptide by peptide synthesis; therefore, these variants may be employed as intermediates for producing the full-length polypeptides of the invention.

Polynucleotides

[0047] Another aspect of the invention relates to isolated polynucleotides, including the full length gene, that encode the histidine kinase polypeptide having the deduced amino acid sequence of Table 1 [SEQ ID NO:2] and polynucleotides closely related thereto and variants thereof.

[0048] Using the information provided herein, such as the polynucleotide sequence set out in Table 1 [SEQ ID NO:1], a polynucleotide of the invention encoding the histidine kinase polypeptide may be obtained using standard cloning and screening methods, such as those for cloning and sequencing chromosomal DNA fragments from bacteria using *Streptococcus pneumoniae* 0100993 cells as starting material, followed by obtaining a full length clone. For example, to obtain a polynucleotide sequence of the invention, such as the sequence given in Table 1 [SEQ ID NO:1], typically

a library of clones of chromosomal DNA of *Streptococcus pneumoniae* 0100993 in *E. coli* or some other suitable host is probed with a radiolabeled oligonucleotide, preferably a 17-mer or longer, derived from a partial sequence. Clones carrying DNA identical to that of the probe can then be distinguished using stringent conditions. By sequencing the individual clones thus identified with sequencing primers designed from the original sequence it is then possible to extend the sequence in both directions to determine the full gene sequence. Conveniently, such sequencing is performed using denatured double stranded DNA prepared from a plasmid clone. Suitable techniques are described by Maniatis, T., Fritsch, E.F. and Sambrook et al., *MOLECULAR CLONING, A LABORATORY MANUAL*, 2nd Ed.; Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York (1989). (see in particular Screening By Hybridization 1.90 and Sequencing Denatured Double-Stranded DNA Templates 13.70). Illustrative of the invention, the polynucleotide set out in Table 1 [SEQ ID NO:1] was discovered in a DNA library derived from *Streptococcus pneumoniae* 0100993.

[0049] The DNA sequence set out in Table 1 [SEQ ID NO:1] contains an open reading frame encoding a protein having about the number of amino acid residues set forth in Table 1 [SEQ ID NO:2] with a deduced molecular weight that can be calculated using amino acid residue molecular weight values well known in the art. The polynucleotide of SEQ ID NO: 1, between nucleotide number 450 through number 2129 encodes the polypeptide of SEQ ID NO:2. The stop codon begins at nucleotide number 2130 of SEQ ID NO:1.

[0050] The histidine kinase of the invention is structurally related to other proteins of the histidine kinase family, as shown by the results of sequencing the DNA encoding histidine kinase of the deposited strain. The protein exhibits greatest homology to lytS from *Bacillus subtilis* protein among known proteins. The histidine kinase of Table 1 [SEQ ID NO:2] has about 21% identity over its entire length and about 50% similarity over its entire length with the amino acid sequence of lytS from *Bacillus subtilis* polypeptide.

[0051] The invention provides a polynucleotide sequence identical over its entire length to the coding sequence in Table 1 [SEQ ID NO:1]. Also provided by the invention is the coding sequence for the mature polypeptide or a fragment thereof, by itself as well as the coding sequence for the mature polypeptide or a fragment in reading frame with other coding sequence, such as those encoding a leader or secretory sequence, a pre-, or pro- or prepro- protein sequence. The polynucleotide may also contain non-coding sequences, including for example, but not limited to non-coding 5' and 3' sequences, such as the transcribed, non-translated sequences, termination signals, ribosome binding sites, sequences that stabilize mRNA, introns, polyadenylation signals, and additional coding sequence which encode additional amino acids. For example, a marker sequence that facilitates purification of the fused polypeptide can be encoded. In certain embodiments of the invention, the marker sequence is a hexa-histidine peptide, as provided in the pQE vector (Qiagen, Inc.) and described in Gentz *et al.*, *Proc. Natl. Acad. Sci., USA* 86: 821-824 (1989), or an HA tag (Wilson *et al.*, *Cell* 37: 767 (1984). Polynucleotides of the invention also include, but are not limited to, polynucleotides comprising a structural gene and its naturally associated sequences that control gene expression.

[0052] A preferred embodiment of the invention is the polynucleotide of comprising nucleotide 450 to 2129 set forth in SEQ ID NO: 1 of Table 1 which encodes the histidine kinase polypeptide.

[0053] The invention also includes polynucleotides of the formula set forth in Table 1 (C) wherein, at the 5' end of the molecule, X is hydrogen, and at the 3' end of the molecule, Y is hydrogen or a metal, R₁ and R₂ is any nucleic acid residue, and n is an integer between 1 and 1000. Any stretch of nucleic acid residues denoted by either R group, where R is greater than 1, may be either a heteropolymer or a homopolymer, preferably a heteropolymer.

[0054] The term "polynucleotide encoding a polypeptide" as used herein encompasses polynucleotides that include a sequence encoding a polypeptide of the invention, particularly a bacterial polypeptide and more particularly a polypeptide of the *Streptococcus pneumoniae* histidine kinase having the amino acid sequence set out in Table 1 [SEQ ID NO: 2]. The term also encompasses polynucleotides that include a single continuous region or discontinuous regions encoding the polypeptide (for example, interrupted by integrated phage or an insertion sequence or editing) together with additional regions, that also may contain coding and/or non-coding sequences.

[0055] The invention further relates to variants of the polynucleotides described herein that encode for variants of the polypeptide having the deduced amino acid sequence of Table 1 [SEQ ID NO:2]. Variants that are fragments of the polynucleotides of the invention may be used to synthesize full-length polynucleotides of the invention.

[0056] Further particularly preferred embodiments are polynucleotides encoding histidine kinase variants, that have the amino acid sequence of histidine kinase polypeptide of Table 1 [SEQ ID NO:2] in which several, a few, 5 to 10, 1 to 5, 1 to 3, 2, 1 or no amino acid residues are substituted, deleted or added, in any combination. Especially preferred among these are silent substitutions, additions and deletions, that do not alter the properties and activities of histidine kinase.

[0057] Further preferred embodiments of the invention are polynucleotides that are at least 70% identical over their entire length to a polynucleotide encoding histidine kinase polypeptide having the amino acid sequence set out in Table 1 [SEQ ID NO:2], and polynucleotides that are complementary to such polynucleotides. Alternatively, most highly preferred are polynucleotides that comprise a region that is at least 80% identical over its entire length to a polynucleotide encoding histidine kinase polypeptide of the deposited strain and polynucleotides complementary thereto. In this re-

gard, polynucleotides at least 90% identical over their entire length to the same are particularly preferred, and among these particularly preferred polynucleotides, those with at least 95% are especially preferred. Furthermore, those with at least 97% are highly preferred among those with at least 95%, and among these those with at least 98% and at least 99% are particularly highly preferred, with at least 99% being the more preferred.

5 [0058] Preferred embodiments are polynucleotides that encode polypeptides that retain substantially the same biological function or activity as the mature polypeptide encoded by the DNA of Table 1 [SEQ ID NO:1].

[0059] The invention further relates to polynucleotides that hybridize to the herein above-described sequences. In this regard, the invention especially relates to polynucleotides that hybridize under stringent conditions to the herein above-described polynucleotides. As herein used, the terms "stringent conditions" and "stringent hybridization conditions" mean hybridization will occur only if there is at least 95% and preferably at least 97% identity between the sequences. An example of stringent hybridization conditions is overnight incubation at 42°C in a solution comprising: 10 50% formamide, 5x SSC (150mM NaCl, 15mM trisodium citrate), 50 mM sodium phosphate (pH7.6), 5x Denhardt's solution, 10% dextran sulfate, and 20 micrograms/ml denatured, sheared salmon sperm DNA, followed by washing the hybridization support in 0.1x SSC at about 65°C. Hybridization and wash conditions are well known and exemplified in Sambrook, *et al.*, Molecular Cloning: A Laboratory Manual, Second Edition, Cold Spring Harbor, N.Y., (1989), particularly Chapter 11 therein.

[0060] The invention also provides a polynucleotide consisting essentially of a polynucleotide sequence obtainable by screening an appropriate library containing the complete gene for a polynucleotide sequence set forth in SEQ ID NO:1 under stringent hybridization conditions with a probe having the sequence of said polynucleotide sequence set forth in SEQ ID NO: 1 or a fragment thereof; and isolating said DNA sequence. Fragments useful for obtaining such a polynucleotide include, for example, probes and primers described elsewhere herein.

[0061] As discussed additionally herein regarding polynucleotide assays of the invention, for instance, polynucleotides of the invention as discussed above, may be used as a hybridization probe for RNA, cDNA and genomic DNA to isolate full-length cDNAs and genomic clones encoding histidine kinase and to isolate cDNA and genomic clones of other genes that have a high sequence similarity to the histidine kinase gene. Such probes generally will comprise at least 15 bases. Preferably, such probes will have at least 30 bases and may have at least 50 bases. Particularly preferred probes will have at least 30 bases and will have 50 bases or less.

[0062] For example, the coding region of the histidine kinase gene may be isolated by screening using the DNA sequence provided in SEQ ID NO: 1 to synthesize an oligonucleotide probe. A labeled oligonucleotide having a sequence complementary to that of a gene of the invention is then used to screen a library of cDNA, genomic DNA or mRNA to determine which members of the library the probe hybridizes to.

[0063] The polynucleotides and polypeptides of the invention may be employed, for example, as research reagents and materials for discovery of treatments of and diagnostics for disease, particularly human disease, as further discussed herein relating to polynucleotide assays.

35 [0064] Polynucleotides of the invention that are oligonucleotides derived from the sequences of SEQ ID NOS: 1 and/or 2 may be used in the processes herein as described, but preferably for PCR, to determine whether or not the polynucleotides identified herein in whole or in part are transcribed in bacteria in infected tissue. It is recognized that such sequences will also have utility in diagnosis of the stage of infection and type of infection the pathogen has attained.

[0065] The invention also provides polynucleotides that may encode a polypeptide that is the mature protein plus additional amino or carboxyl-terminal amino acids, or amino acids interior to the mature polypeptide (when the mature form has more than one polypeptide chain, for instance). Such sequences may play a role in processing of a protein from precursor to a mature form, may allow protein transport, may lengthen or shorten protein half-life or may facilitate manipulation of a protein for assay or production, among other things. As generally is the case *in vivo*, the additional amino acids may be processed away from the mature protein by cellular enzymes.

45 [0066] A precursor protein, having the mature form of the polypeptide fused to one or more prosequences may be an inactive form of the polypeptide. When prosequences are removed such inactive precursors generally are activated. Some or all of the prosequences may be removed before activation. Generally, such precursors are called preproteins.

[0067] In sum, a polynucleotide of the invention may encode a mature protein, a mature protein plus a leader sequence (which may be referred to as a preprotein), a precursor of a mature protein having one or more prosequences that are not the leader sequences of a preprotein, or a preproprotein, which is a precursor to a preprotein, having a leader sequence and one or more prosequences, which generally are removed during processing steps that produce active and mature forms of the polypeptide.

Vectors, hosts, expression

55 [0068] The invention also relates to vectors that comprise a polynucleotide or polynucleotides of the invention, host cells that are genetically engineered with vectors of the invention and the production of polypeptides of the invention by recombinant techniques. Cell-free translation systems can also be employed to produce such proteins using RNAs

derived from the DNA constructs of the invention.

[0069] For recombinant production, host cells can be genetically engineered to incorporate expression systems or portions thereof or polynucleotides of the invention. Introduction of a polynucleotide into the host cell can be effected by methods described in many standard laboratory manuals, such as Davis et al., *BASIC METHODS IN MOLECULAR BIOLOGY*, (1986) and Sambrook et al., *MOLECULAR CLONING: A LABORATORY MANUAL*, 2nd Ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. (1989), such as, calcium phosphate transfection, DEAE-dextran mediated transfection, transfection, microinjection, cationic lipid-mediated transfection, electroporation, transduction, scrape loading, ballistic introduction and infection.

[0070] Representative examples of appropriate hosts include bacterial cells, such as streptococci, staphylococci, enterococci *E. coli*, streptomyces and *Bacillus subtilis* cells; fungal cells, such as yeast cells and *Aspergillus* cells; insect cells such as *Drosophila* S2 and *Spodoptera* Sf9 cells; animal cells such as CHO, COS, HeLa, C127, 3T3, BHK, 293 and Bowes melanoma cells; and plant cells.

[0071] A great variety of expression systems can be used to produce the polypeptides of the invention. Such vectors include, among others, chromosomal, episomal and virus-derived vectors, e.g., vectors derived from bacterial plasmids, from bacteriophage, from transposons, from yeast episomes, from insertion elements, from yeast chromosomal elements, from viruses such as baculoviruses, papova viruses, such as SV40, vaccinia viruses, adenoviruses, fowl pox viruses, pseudorabies viruses and retroviruses, and vectors derived from combinations thereof, such as those derived from plasmid and bacteriophage genetic elements, such as cosmids and phagemids. The expression system constructs may contain control regions that regulate as well as engender expression. Generally, any system or vector suitable to maintain, propagate or express polynucleotides and/or to express a polypeptide in a host may be used for expression in this regard. The appropriate DNA sequence may be inserted into the expression system by any of a variety of well-known and routine techniques, such as, for example, those set forth in Sambrook et al., *MOLECULAR CLONING, A LABORATORY MANUAL*, (*supra*).

[0072] For secretion of the translated protein into the lumen of the endoplasmic reticulum, into the periplasmic space or into the extracellular environment, appropriate secretion signals may be incorporated into the expressed polypeptide. These signals may be endogenous to the polypeptide or they may be heterologous signals.

[0073] Polypeptides of the invention can be recovered and purified from recombinant cell cultures by well-known methods including ammonium sulfate or ethanol precipitation, acid extraction, anion or cation exchange chromatography, phosphocellulose chromatography, hydrophobic interaction chromatography, affinity chromatography, hydroxylapatite chromatography, and lectin chromatography. Most preferably, high performance liquid chromatography is employed for purification. Well known techniques for refolding protein may be employed to regenerate active conformation when the polypeptide is denatured during isolation and or purification.

Diagnostic Assays

[0074] This invention is also related to the use of the histidine kinase polynucleotides of the invention for use as diagnostic reagents. Detection of histidine kinase in a eukaryote, particularly a mammal, and especially a human, will provide a diagnostic method for diagnosis of a disease. Eukaryotes (herein also "individual(s)"), particularly mammals, and especially humans, particularly those infected or suspected to be infected with an organism comprising the histidine kinase gene may be detected at the nucleic acid level by a variety of techniques.

[0075] Nucleic acids for diagnosis may be obtained from an infected individual's cells and tissues, such as bone, blood, muscle, cartilage, and skin. Genomic DNA may be used directly for detection or may be amplified enzymatically by using PCR or other amplification technique prior to analysis. RNA or cDNA may also be used in the same ways. Using amplification, characterization of the species and strain of prokaryote present in an individual, may be made by an analysis of the genotype of the prokaryote gene. Deletions and insertions can be detected by a change in size of the amplified product in comparison to the genotype of a reference sequence. Point mutations can be identified by hybridizing amplified DNA to labeled histidine kinase polynucleotide sequences. Perfectly matched sequences can be distinguished from mismatched duplexes by RNase digestion or by differences in melting temperatures. DNA sequence differences may also be detected by alterations in the electrophoretic mobility of the DNA fragments in gels, with or without denaturing agents, or by direct DNA sequencing. See, e.g., Myers et al., *Science*, 230: 1242 (1985). Sequence changes at specific locations also may be revealed by nuclease protection assays, such as RNase and S1 protection or a chemical cleavage method. See, e.g., Cotton et al., *Proc. Natl. Acad. Sci., USA*, 85: 4397-4401 (1985).

[0076] Cells carrying mutations or polymorphisms in the gene of the invention may also be detected at the DNA level by a variety of techniques, to allow for serotyping, for example. For example, RT-PCR can be used to detect mutations. It is particularly preferred to use RT-PCR in conjunction with automated detection systems, such as, for example, GeneScan. RNA or cDNA may also be used for the same purposes, PCR or RT-PCR. As an example, PCR primers complementary to a nucleic acid encoding histidine kinase can be used to identify and analyze mutations. Examples of representative primers are shown below in Table 2.

Table 2

Primers for amplification of Histidine kinase polynucleotides

<u>SEQ ID NO</u>	<u>PRIMER SEQUENCE</u>
3	5' -ATGAAATCATCCATGAAAAATTGG-3'
4	5' -CTCATCTTGAATTGTAATACGATA-3'

[0077] The invention further provides these primers with 1, 2, 3 or 4 nucleotides removed from the 5' and/or the 3' end. These primers may be used for, among other things, amplifying histidine kinase DNA isolated from a sample derived from an individual. The primers may be used to amplify the gene isolated from an infected individual such that the gene may then be subject to various techniques for elucidation of the DNA sequence. In this way, mutations in the DNA sequence may be detected and used to diagnose infection and to serotype and/or classify the infectious agent.

[0078] The invention further provides a process for diagnosing, disease, preferably bacterial infections, more preferably infections by *Streptococcus pneumoniae*, and most preferably otitis media, conjunctivitis, pneumonia, bacteremia, meningitis, sinusitis, pleural empyema and endocarditis, and most particularly meningitis, such as for example infection of cerebrospinal fluid, comprising determining from a sample derived from an individual a increased level of expression of polynucleotide having the sequence of Table 1 [SEQ ID NO: 1]. Increased or decreased expression of histidine kinase polynucleotide can be measured using any one of the methods well known in the art for the quantitation of polynucleotides, such as, for example, amplification, PCR, RT-PCR, RNase protection, Northern blotting and other hybridization methods.

[0079] In addition, a diagnostic assay in accordance with the invention for detecting over-expression of histidine kinase protein compared to normal control tissue samples may be used to detect the presence of an infection, for example. Assay techniques that can be used to determine levels of a histidine kinase protein, in a sample derived from a host are well-known to those of skill in the art. Such assay methods include radioimmunoassays, competitive-binding assays, Western Blot analysis and ELISA assays.

Antibodies

[0080] The polypeptides of the invention or variants thereof, or cells expressing them can be used as an immunogen to produce antibodies immunospecific for such polypeptides. "Antibodies" as used herein includes monoclonal and polyclonal antibodies, chimeric, single chain, simianized antibodies and humanized antibodies, as well as Fab fragments, including the products of an Fab immunoglobulin expression library.

[0081] Antibodies generated against the polypeptides of the invention can be obtained by administering the polypeptides or epitope-bearing fragments, analogues or cells to an animal, preferably a nonhuman, using routine protocols. For preparation of monoclonal antibodies, any technique known in the art that provides antibodies produced by continuous cell line cultures can be used. Examples include various techniques, such as those in Kohler, G. and Milstein, C., *Nature* 256: 495-497 (1975); Kozbor *et al.*, *Immunology Today* 4: 72 (1983); Cole *et al.*, pg. 77-96 in *MONOCLONAL ANTIBODIES AND CANCER THERAPY*, Alan R. Liss, Inc. (1985).

[0082] Techniques for the production of single chain antibodies (U.S. Patent No. 4,946,778) can be adapted to produce single chain antibodies to polypeptides of this invention. Also, transgenic mice, or other organisms such as other mammals, may be used to express humanized antibodies.

[0083] Alternatively phage display technology may be utilized to select antibody genes with binding activities towards the polypeptide either from repertoires of PCR amplified v-genes of lymphocytes from humans screened for possessing anti-histidine kinase or from naive libraries (McCafferty, J. *et al.*, (1990), *Nature* 348, 552-554; Marks, J. *et al.*, (1992) *Biotechnology* 10, 779-783). The affinity of these antibodies can also be improved by chain shuffling (Clackson, T. *et al.*, (1991) *Nature* 352, 624-628).

[0084] If two antigen binding domains are present each domain may be directed against a different epitope - termed 'bispecific' antibodies.

[0085] The above-described antibodies may be employed to isolate or to identify clones expressing the polypeptides to purify the polypeptides by affinity chromatography.

[0086] Thus, among others, antibodies against histidine kinase- polypeptide may be employed to treat infections,

particularly bacterial infections and especially otitis media, conjunctivitis, pneumonia, bacteremia, meningitis, sinusitis, pleural empyema and endocarditis, and most particularly meningitis, such as for example infection of cerebrospinal fluid.

[0087] Polypeptide variants include antigenically, epitopically or immunologically equivalent variants that form a particular aspect of this invention. The term "antigenically equivalent derivative" as used herein encompasses a polypeptide or its equivalent which will be specifically recognized by certain antibodies which, when raised to the protein or polypeptide according to the invention, interfere with the immediate physical interaction between pathogen and mammalian host. The term "immunologically equivalent derivative" as used herein encompasses a peptide or its equivalent which when used in a suitable formulation to raise antibodies in a vertebrate, the antibodies act to interfere with the immediate physical interaction between pathogen and mammalian host.

[0088] The polypeptide, such as an antigenically or immunologically equivalent derivative or a fusion protein thereof is used as an antigen to immunize a mouse or other animal such as a rat or chicken. The fusion protein may provide stability to the polypeptide. The antigen may be associated, for example by conjugation, with an immunogenic carrier protein for example bovine serum albumin (BSA) or keyhole limpet haemocyanin (KLH). Alternatively a multiple antigenic peptide comprising multiple copies of the protein or polypeptide, or an antigenically or immunologically equivalent polypeptide thereof may be sufficiently antigenic to improve immunogenicity so as to obviate the use of a carrier.

[0089] Preferably, the antibody or variant thereof is modified to make it less immunogenic in the individual. For example, if the individual is human the antibody may most preferably be "humanized"; where the complementarity determining region(s) of the hybridoma-derived antibody has been transplanted into a human monoclonal antibody, for example as described in Jones, P. et al. (1986), *Nature* 321, 522-525 or Tempest et al., (1991) *Biotechnology* 9, 266-273.

[0090] The use of a polynucleotide of the invention in genetic immunization will preferably employ a suitable delivery method such as direct injection of plasmid DNA into muscles (Wolff et al., *Hum Mol Genet* 1992, 1:363, Manthorpe et al., *Hum. Gene Ther.* 1993, 4, 419), delivery of DNA complexed with specific protein carriers (Wu et al., *J Biol Chem.* 1989: 264,16985), coprecipitation of DNA with calcium phosphate (Benvenisty & Reshef, *PNAS USA*, 1986:83,9551), encapsulation of DNA in various forms of liposomes (Kaneda et al., *Science* 1989:243,375), particle bombardment (Tang et al., *Nature* 1992, 356:152, Eisenbraun et al., *DNA Cell Biol* 1993, 12:791) and *in vivo* infection using cloned retroviral vectors (Seeger et al., *PNAS USA* 1984:81,5849).

Antagonists and agonists - assays and molecules

[0091] Polypeptides of the invention may also be used to assess the binding of small molecule substrates and ligands in, for example, cells, cell-free preparations, chemical libraries, and natural product mixtures. These substrates and ligands may be natural substrates and ligands or may be structural or functional mimetics. See, e.g., Coligan et al., *Current Protocols in Immunology* 1(2): Chapter 5 (1991).

[0092] The invention also provides a method of screening compounds to identify those which enhance (agonist) or block (antagonist) the action of histidine kinase polypeptides or polynucleotides, particularly those compounds that are bacteriostatic and/or bacteriocidal. The method of screening may involve high-throughput techniques. For example, to screen for agonists or antagonists, a synthetic reaction mix, a cellular compartment, such as a membrane, cell envelope or cell wall, or a preparation of any thereof, comprising histidine kinase polypeptide and a labeled substrate or ligand of such polypeptide is incubated in the absence or the presence of a candidate molecule that may be a histidine kinase agonist or antagonist. The ability of the candidate molecule to agonize or antagonize the histidine kinase polypeptide is reflected in decreased binding of the labeled ligand or decreased production of product from such substrate. Molecules that bind gratuitously, i.e., without inducing the effects of histidine kinase polypeptide are most likely to be good antagonists. Molecules that bind well and increase the rate of product production from substrate are agonists. Detection of the rate or level of production of product from substrate may be enhanced by using a reporter system. Reporter systems that may be useful in this regard include but are not limited to colorimetric labeled substrate converted into product, a reporter gene that is responsive to changes in histidine kinase polynucleotide or polypeptide activity, and binding assays known in the art.

[0093] Another example of an assay for histidine kinase antagonists is a competitive assay that combines histidine kinase and a potential antagonist with histidine kinase-binding molecules, recombinant histidine kinase binding molecules, natural substrates or ligands, or substrate or ligand mimetics, under appropriate conditions for a competitive inhibition assay. The histidine kinase molecule can be labeled, such as by radioactivity or a colorimetric compound, such that the number of histidine kinase molecules bound to a binding molecule or converted to product can be determined accurately to assess the effectiveness of the potential antagonist.

[0094] Potential antagonists include small organic molecules, peptides, polypeptides and antibodies that bind to a polynucleotide or polypeptide of the invention and thereby inhibit or extinguish its activity. Potential antagonists also may be small organic molecules, a peptide, a polypeptide such as a closely related protein or antibody that binds the same sites on a binding molecule, such as a binding molecule, without inducing histidine kinase-induced activities,

thereby preventing the action of histidine kinase by excluding histidine kinase from binding.

[0095] Potential antagonists include a small molecule that binds to and occupies the binding site of the polypeptide thereby preventing binding to cellular binding molecules, such that normal biological activity is prevented. Examples of small molecules include but are not limited to small organic molecules, peptides or peptide-like molecules. Other potential antagonists include antisense molecules (see Okano, *J. Neurochem.* 56: 560 (1991); *OLIGODEOXYNUCLEOTIDES AS ANTISENSE INHIBITORS OF GENE EXPRESSION*, CRC Press, Boca Raton, FL (1988), for a description of these molecules). Preferred potential antagonists include compounds related to and variants of histidine kinase.

[0096] Each of the DNA sequences provided herein may be used in the discovery and development of antibacterial compounds. The encoded protein, upon expression, can be used as a target for the screening of antibacterial drugs.

Additionally, the DNA sequences encoding the amino terminal regions of the encoded protein or Shine-Delgarno or other translation facilitating sequences of the respective mRNA can be used to construct antisense sequences to control the expression of the coding sequence of interest.

[0097] The invention also provides the use of the polypeptide, polynucleotide or inhibitor of the invention to interfere with the initial physical interaction between a pathogen and mammalian host responsible for sequelae of infection. In particular the molecules of the invention may be used: in the prevention of adhesion of bacteria, in particular gram positive bacteria, to mammalian extracellular matrix proteins on in-dwelling devices or to extracellular matrix proteins in wounds; to block histidine kinase protein-mediated mammalian cell invasion by, for example, initiating phosphorylation of mammalian tyrosine kinases (Rosenshine *et al.*, *Infect. Immun.* 60:2211 (1992); to block bacterial adhesion between mammalian extracellular matrix proteins and bacterial histidine kinase proteins that mediate tissue damage and; to block the normal progression of pathogenesis in infections initiated other than by the implantation of in-dwelling devices or by other surgical techniques.

[0098] This invention provides a method of screening drugs to identify those which interfere with i) the interaction of the histidine kinase with a response regulator, the method comprising incubating the histidine kinase with response regulator in the presence of the drug and measuring the ability of the drug to block this interaction; and/or ii) the ability of the histidine kinase to autophosphorylate, the method comprising incubating the histidine kinase with the drug and measuring the ability of the drug to prevent autophosphorylation.

[0099] The response regulator is preferably the cognate response regulator of the histidine kinase, or another response regulator which is capable of using the histidine kinase as a substrate, and is preferably from *Streptococcus pneumoniae* or another microorganism e.g. *Bacillus*. Generally the genes for a histidine kinase and its cognate response regulator are found close together on the chromosome so a suitable histidine kinase may conveniently be identified by further sequencing along the chromosome. The invention also relates to inhibitors identified thereby.

[0100] The antagonists and agonists of the invention may be employed, for instance, to inhibit and treat otitis media, conjunctivitis, pneumonia, bacteremia, meningitis, sinusitis, pleural empyema and endocarditis, and most particularly meningitis, such as for example infection of cerebrospinal fluid.

[0101] *Helicobacter pylori* (herein *H. pylori*) bacteria infect the stomachs of over one-third of the world's population causing stomach cancer, ulcers, and gastritis (International Agency for Research on Cancer (1994) Schistosomes, Liver Flukes and *Helicobacter Pylori* (International Agency for Research on Cancer, Lyon, France; <http://www.uicc.ch/ecp/ecp2904.htm>). Moreover, the international Agency for Research on Cancer recently recognized a cause-and-effect relationship between *H. pylori* and gastric adenocarcinoma, classifying the bacterium as a Group I (definite) carcinogen.

Preferred antimicrobial compounds of the invention (agonists and antagonists of histidine kinase) found using screens provided by the invention, particularly broad-spectrum antibiotics, should be useful in the treatment of *H. pylori* infection. Such treatment should decrease the advent of *H. pylori*-induced cancers, such as gastrointestinal carcinoma. Such treatment should also cure gastric ulcers and gastritis.

Vaccines

[0102] Another aspect of the invention relates to a method for inducing an immunological response in an individual, particularly a mammal which comprises inoculating the individual with histidine kinase, or a fragment or variant thereof, adequate to produce antibody and/ or T cell immune response to protect said individual from infection, particularly bacterial infection and most particularly *Streptococcus pneumoniae* infection. Also provided are methods whereby such immunological response slows bacterial replication. Yet another aspect of the invention relates to a method of inducing immunological response in an individual which comprises delivering to such individual a nucleic acid vector to direct expression of histidine kinase, or a fragment or a variant thereof, for expressing histidine kinase, or a fragment or a variant thereof *in vivo* in order to induce an immunological response, such as, to produce antibody and/ or T cell immune response, including, for example, cytokine-producing T cells or cytotoxic T cells, to protect said individual from disease, whether that disease is already established within the individual or not. One way of administering the gene is by accelerating it into the desired cells as a coating on particles or otherwise.

[0103] Such nucleic acid vector may comprise DNA, RNA, a modified nucleic acid, or a DNA/RNA hybrid.

[0104] A further aspect of the invention relates to an immunological composition which, when introduced into an individual capable or having induced within it an immunological response, induces an immunological response in such individual to a histidine kinase or protein coded therefrom, wherein the composition comprises a recombinant histidine kinase or protein coded therefrom comprising DNA which codes for and expresses an antigen of said histidine kinase or protein coded therefrom. The immunological response may be used therapeutically or prophylactically and may take the form of antibody immunity or cellular immunity such as that arising from CTL or CD4+ T cells.

[0105] A histidine kinase polypeptide or a fragment thereof may be fused with co-protein which may not by itself produce antibodies, but is capable of stabilizing the first protein and producing a fused protein which will have immunogenic and protective properties. Thus fused recombinant protein, preferably further comprises an antigenic co-protein, such as lipoprotein D from *Hemophilus influenzae*, Glutathione-S-transferase (GST) or beta-galactosidase, relatively large co-proteins which solubilize the protein and facilitate production and purification thereof. Moreover, the co-protein may act as an adjuvant in the sense of providing a generalized stimulation of the immune system. The co-protein may be attached to either the amino or carboxy terminus of the first protein.

[0106] Provided by this invention are compositions, particularly vaccine compositions, and methods comprising the polypeptides or polynucleotides of the invention and immunostimulatory DNA sequences, such as those described in Sato, Y. *et al. Science* 273: 352 (1996).

[0107] Also, provided by this invention are methods using the described polynucleotide or particular fragments thereof which have been shown to encode non-variable regions of bacterial cell surface proteins in DNA constructs used in such genetic immunization experiments in animal models of infection with *Streptococcus pneumoniae* will be particularly useful for identifying protein epitopes able to provoke a prophylactic or therapeutic immune response. It is believed that this approach will allow for the subsequent preparation of monoclonal antibodies of particular value from the requisite organ of the animal successfully resisting or clearing infection for the development of prophylactic agents or therapeutic treatments of bacterial infection, particularly *Streptococcus pneumoniae* infection, in mammals, particularly humans.

[0108] The polypeptide may be used as an antigen for vaccination of a host to produce specific antibodies which protect against invasion of bacteria, for example by blocking adherence of bacteria to damaged tissue. Examples of tissue damage include wounds in skin or connective tissue caused, e.g., by mechanical, chemical or thermal damage or by implantation of indwelling devices, or wounds in the mucous membranes, such as the mouth, mammary glands, urethra or vagina.

[0109] The invention also includes a vaccine formulation which comprises an immunogenic recombinant protein of the invention together with a suitable carrier. Since the protein may be broken down in the stomach, it is preferably administered parenterally, including, for example, administration that is subcutaneous, intramuscular, intravenous, or intradermal. Formulations suitable for parenteral administration include aqueous and non-aqueous sterile injection solutions which may contain anti-oxidants, buffers, bacteriostats and solutes which render the formulation isotonic with the bodily fluid, preferably the blood, of the individual; and aqueous and non-aqueous sterile suspensions which may include suspending agents or thickening agents. The formulations may be presented in unit-dose or multi-dose containers, for example, sealed ampules and vials and may be stored in a freeze-dried condition requiring only the addition of the sterile liquid carrier immediately prior to use. The vaccine formulation may also include adjuvant systems for enhancing the immunogenicity of the formulation, such as oil-in water systems and other systems known in the art.

The dosage will depend on the specific activity of the vaccine and can be readily determined by routine experimentation.

[0110] While the invention has been described with reference to certain histidine kinase protein, it is to be understood that this covers fragments of the naturally occurring protein and similar proteins with additions, deletions or substitutions which do not substantially affect the immunogenic properties of the recombinant protein.

Compositions, kits and administration

[0111] The invention also relates to compositions comprising the polynucleotide or the polypeptides discussed above or their agonists or antagonists. The polypeptides of the invention may be employed in combination with a non-sterile or sterile carrier or carriers for use with cells, tissues or organisms, such as a pharmaceutical carrier suitable for administration to a subject. Such compositions comprise, for instance, a media additive or a therapeutically effective amount of a polypeptide of the invention and a pharmaceutically acceptable carrier or excipient. Such carriers may include, but are not limited to, saline, buffered saline, dextrose, water, glycerol, ethanol and combinations thereof. The formulation should suit the mode of administration. The invention further relates to diagnostic and pharmaceutical packs and kits comprising one or more containers filled with one or more of the ingredients of the aforementioned compositions of the invention.

[0112] Polypeptides and other compounds of the invention may be employed alone or in conjunction with other compounds, such as therapeutic compounds.

[0113] The pharmaceutical compositions may be administered in any effective, convenient manner including, for

instance, administration by topical, oral, anal, vaginal, intravenous, intraperitoneal, intramuscular, subcutaneous, intranasal or intradermal routes among others.

[0114] In therapy or as a prophylactic, the active agent may be administered to an individual as an injectable composition, for example as a sterile aqueous dispersion, preferably isotonic.

[0115] Alternatively the composition may be formulated for topical application for example in the form of ointments, creams, lotions, eye ointments, eye drops, ear drops, mouthwash, impregnated dressings and sutures and aerosols, and may contain appropriate conventional additives, including, for example, preservatives, solvents to assist drug penetration, and emollients in ointments and creams. Such topical formulations may also contain compatible conventional carriers, for example cream or ointment bases, and ethanol or oleyl alcohol for lotions. Such carriers may constitute from about 1% to about 98% by weight of the formulation; more usually they will constitute up to about 80% by weight of the formulation.

[0116] For administration to mammals, and particularly humans, it is expected that the daily dosage level of the active agent will be from 0.01 mg/kg to 10 mg/kg, typically around 1 mg/kg. The physician in any event will determine the actual dosage which will be most suitable for an individual and will vary with the age, weight and response of the particular individual. The above dosages are exemplary of the average case. There can, of course, be individual instances where higher or lower dosage ranges are merited, and such are within the scope of this invention.

[0117] In-dwelling devices include surgical implants, prosthetic devices and catheters, i.e., devices that are introduced to the body of an individual and remain in position for an extended time. Such devices include, for example, artificial joints, heart valves, pacemakers, vascular grafts, vascular catheters, cerebrospinal fluid shunts, urinary catheters, continuous ambulatory peritoneal dialysis (CAPD) catheters.

[0118] The composition of the invention may be administered by injection to achieve a systemic effect against relevant bacteria shortly before insertion of an in-dwelling device. Treatment may be continued after surgery during the in-body time of the device. In addition, the composition could also be used to broaden perioperative cover for any surgical technique to prevent bacterial wound infections, especially *Streptococcus pneumoniae* wound infections.

[0119] Many orthopaedic surgeons consider that humans with prosthetic joints should be considered for antibiotic prophylaxis before dental treatment that could produce a bacteremia. Late deep infection is a serious complication sometimes leading to loss of the prosthetic joint and is accompanied by significant morbidity and mortality. It may therefore be possible to extend the use of the active agent as a replacement for prophylactic antibiotics in this situation.

[0120] In addition to the therapy described above, the compositions of this invention may be used generally as a wound treatment agent to prevent adhesion of bacteria to matrix proteins exposed in wound tissue and for prophylactic use in dental treatment as an alternative to, or in conjunction with, antibiotic prophylaxis.

[0121] Alternatively, the composition of the invention may be used to bathe an indwelling device immediately before insertion. The active agent will preferably be present at a concentration of 1µg/ml to 10mg/ml for bathing of wounds or indwelling devices.

[0122] A vaccine composition is conveniently in injectable form. Conventional adjuvants may be employed to enhance the immune response. A suitable unit dose for vaccination is 0.5-5 microgram/kg of antigen, and such dose is preferably administered 1-3 times and with an interval of 1-3 weeks. With the indicated dose range, no adverse toxicological effects will be observed with the compounds of the invention which would preclude their administration to suitable individuals.

[0123] Each reference disclosed herein is incorporated by reference herein in its entirety. Any patent application to which this application claims priority is also incorporated by reference herein in its entirety.

EXAMPLES

[0124] The examples below are carried out using standard techniques, which are well known and routine to those of skill in the art, except where otherwise described in detail. The examples are illustrative, but do not limit the invention.

Example 1 Strain selection, Library Production and Sequencing

[0125] The polynucleotide having the DNA sequence given in SEQ ID NO:1 was obtained from a library of clones of chromosomal DNA of *Streptococcus pneumoniae* in *E. coli*. The sequencing data from two or more clones containing overlapping *Streptococcus pneumoniae* DNAs was used to construct the contiguous DNA sequence in SEQ ID NO:1. Libraries may be prepared by routine methods, for example: Methods 1 and 2 below.

[0126] Total cellular DNA is isolated from *Streptococcus pneumoniae* 0100993 according to standard procedures and size-fractionated by either of two methods.

Method 1

[0127] Total cellular DNA is mechanically sheared by passage through a needle in order to size-fractionate according to standard procedures. DNA fragments of up to 11 kbp in size are rendered blunt by treatment with exonuclease and DNA polymerase, and EcoRI linkers added. Fragments are ligated into the vector Lambda ZapII that has been cut with EcoRI, the library packaged by standard procedures and *E. coli* infected with the packaged library. The library is amplified by standard procedures.

Method 2

[0128] Total cellular DNA is partially hydrolyzed with a one or a combination of restriction enzymes appropriate to generate a series of fragments for cloning into library vectors (e.g., RsaI, PstI, AluI, BshI235I), and such fragments are size-fractionated according to standard procedures. EcoRI linkers are ligated to the DNA and the fragments then ligated into the vector Lambda ZapII that have been cut with EcoRI, the library packaged by standard procedures, and *E. coli* infected with the packaged library. The library is amplified by standard procedures.

Ann x t the d s r i p t i o n

[0129]

5

SEQUENCE LISTING

10

(1) GENERAL INFORMATION:

(i) APPLICANT:

15

(A) NAME: SmithKline Beecham Corporation

(B) STREET: One Franklin Plaza

(C) CITY: Philadelphia

(D) STATE OR PROVINCE: PA

(E) COUNTRY: USA

20

(F) POSTAL CODE: 19103

(ii) TITLE OF INVENTION: NOVEL Histidine Kinase

25

(iii) NUMBER OF SEQUENCES: 4

(iv) COMPUTER-READABLE FORM:

30

(A) MEDIUM TYPE: Diskette

(B) COMPUTER: IBM Compatible

(C) OPERATING SYSTEM: Windows 95

(D) SOFTWARE: FastSEQ for Windows Version 2.0b

35

(v) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:

40

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

45

(A) LENGTH: 3453 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

55

CTTATATGCA GAACATGGTT ATAGCTTTCG GGAATACAGT TTGAAGGAGG CTTGGTCTCT

60

	TTACAAGCAA	AATTTTATCT	CAAGCAACCT	GATTTTCTAT	AGCTTTTCTAG	GTGTGGGTCT	120
	AGTTTTGACC	TATGGTTTGT	ATCTCTTGGT	GCAATTGCCT	CATCAGACCA	TTGTTTCATTT	180
5	GATTGCGACC	CTTTTGAATG	TCCTAGTAGT	TGCCCTGATC	TTTTTGGCTT	ATACAGTATC	240
	TTTAAATA	CAAGTTTATT	TTGCCTTGTC	CTATCGAAAT	AGTCTCAAAT	TATCCTTGAT	300
	TGGCATCTTT	ATGAGTCTAG	CAGCTGTGGC	TAAGGTTCTC	CTTGGGACTG	TGCTACTTGT	360
	AGCAATTGGT	TACTATATGC	CTGCCCTGCT	ATTTTTTGTA	GGAATTGGGA	TGTGGCATT	420
10	CTTTATCAGT	GATATGTTGG	AACCTGTCTA	TGAAATCATC	CATGAAAAAT	TGGCGACAAA	480
	ATAGAATGAA	GCACTTTTGG	CTACATACGC	TTCTAAGAAC	CTATAGTTCA	GTGATGATCA	540
	TTATCATTGC	GAGTTTTGCA	ATCTTACTCT	CTTACGCTGA	CTGGGATTCA	CGTGAAAAGG	600
	AAGCCCAGAG	AGTAGCCCAG	CGTGTAAGT	CTAGAACAGT	GAGTGAAATT	GAATATTACC	660
15	ATAGAGAGTC	AACCCAGATA	GCTCAGGCTT	TAGTTGAAAA	CCAAGCTCGT	ATTGAGGGAA	720
	TCTATAAATA	CTTTAGCCTT	AGCATGCCAG	ACTATTTTTA	CTGGCAATTA	GAGCGGAAAG	780
	CTTCGCCTTA	TATATCAGTC	TCTCTGTATG	AAAATGTTGA	TGACCTCTAT	GTTGCAAATG	840
20	ATTTTGTAAC	TGGGGTGGCC	ATTGCTTTTC	AAGATTACAA	GGAAGTCTAT	GTTTCTACTA	900
	AAGACAAACG	TAGTGGAGAA	AAAATCAGGG	CTGAGGATTT	CAAACCAGCA	GGAAATAGTT	960
	TTGCCATTCC	AGTGTGAGAT	CCAGTGTGAG	ATCAAGACTT	AGGAGTGATT	TACATCTCCT	1020
	TGGATCCTGC	TGTTTTATAC	CATGCCATTG	ATAATACTAG	AGGTCATACT	CCGATGGCAG	1080
25	TAACAGTGAC	CGAACCTTTT	GATACGGAGA	TTTTTCATAT	TGGTGAGACA	GTTGATAAGG	1140
	AGAGTGAAAA	TTGGCTAGTT	GGCTTAACTT	CTCATGGTTA	TCAGGTTGAG	GTGGCAGTTC	1200
	CCAAAACTT	TGTTTTACAA	GGAACGGTGA	CCAGCTCTGC	TTTGATTGTG	GGCTTGAGCC	1260
	TTCTCTTTAT	TGTCATTCTT	TATCTGACTT	TGAGGCAGAC	CTTTGCTAAT	TATCAAAAGC	1320
30	AGGTAGTGGA	TTTGGTGGAT	TCCATCCAAG	CTATTGCCCA	AGGACAAGAA	GGTCTTCGCA	1380
	TTGATACGCT	TGAAAAGGAT	CAGGAATTGC	TCCTAATCGC	GGAGACGACC	AATGATATGT	1440
	TGGATCGATT	GGAAAAGAAT	ATCCATGATA	TTTACCAGTT	AGAACTCAGT	CAAAAAGATG	1500
	CCAATATGCG	GGCCTTGACG	GCGCAAATCA	ATCCTCATT	TATGTATAAT	ACGCTGGAGT	1560
35	TCTTGCGCAT	GTATGCAGTT	ATGCAGAGTC	AAGATGAGTT	GGCAGATATC	ATTTATGAAT	1620
	TCAGTAGTCT	CTTGCGTAAC	AATATTTCCG	ACGAAAGAGA	GACCCTCCTC	AAACAGGAAT	1680
	TAGAATTTTG	CCGTAAATAC	AGCTATCTCT	GCATGGTTG	CTATCCCAAG	TCCATTGCCT	1740
	ATGGTTTCAA	GATAGATCCA	GAGTTAGAGA	ATATGAAGAT	TCCCAAGTTT	ACCTTGCAAC	1800
40	CGCTGGTAGA	AAACTATTTT	GCGCATGGTG	TTGACCACAG	GCGGACAGAT	AATGTGATTA	1860
	GCATCAAGGC	TCTTAAACAG	GATGGTTTTG	TGAAATTTT	GGTGGTCGAT	AATGGTAGAG	1920
	GAATGTCGGC	TGAAAAGTTG	GCAATATCC	GAGAAAAATT	AAGTCAGAGA	TATTTTGAAC	1980
	ACCAAGCCAG	CTACAGTGAT	CAAAGGCAGT	CTATCGGGAT	TGTCAATGTA	CACGAGCGTT	2040
45	TTGTGCTCTA	TTTTGGAGAC	CGCTATGCCA	TTACTATAGA	GTCTGCAGAG	CAAGCCGGTG	2100
	TTCAGTATCG	TATTACAATT	CAAGATGAGT	AGAAAGGGAG	AAAATGTATA	AAGTATTATT	2160
	AGTAGATGAT	GAGTACATGG	TGACAGAAGG	TCTGAAGCGT	TTGATTCCCT	TTGATAAGTG	2220
	GGATATGGAG	GTCGTCGCAA	CAGTCAGTCA	TGCCGATGAA	GCTCTAGAAT	ATGTTTCAGGA	2280
50	AAATCCTGTC	GATGTCATCA	TTTCCGATGT	CAATATGCCA	GACAAAACAG	GGCTTGATAT	2340
	GATTCCGGAG	ATGAAAGAGA	TCTTACCAGA	TGCTGCCTAT	ATCCTGCTCT	CAGGTTATCA	2400
	GGAGTTTGAT	TATGTAAAAA	GAGCAATGAA	TCTTAGTGTG	GTGGACTATT	TGGTCAAACC	2460

TGTGATAAG GTAGAGCTGG GAAATCTGCT GGAGAAGATT GCAGGTCAGC TCGGCGAGAG 2520
 AGGGAAGAAA AGTCAGACTC TTAGTCAAGA ATTAGACGAG GCTGGATTTG TTAGTTATTT 2580
 5 AGGGGATAAG GAGAATTGGT GGATAGGTCT ATCCAAGGAA AAACAAGGTT CCTTCACCAT 2640
 TCCCTACTAT GTCTTGGGTC AAGCCTGGCA GATTTTCATT TCTGACCAAC CCCTAGATGG 2700
 TTTAGTCGTT ACACCTTTTG AAGCTCCTTA TCAAGAACAT TTTGAACGCT GGAAGCTGAA 2760
 TGCTGAGAAA ACCCTCTTTT ACGGTTCTGT AAATCTGCAG CAGTCTGAGA GTCTCTTTGC 2820
 10 CTATTACGAA CCGATTTATA GGGTTATCAT TCAGGGAAAT CTCAATCAA TCGTAGAAGA 2880
 GTTAAATCTC TTGGAGAAGG TAGTTCCTGA AAATACGCCG CGAATTCCGA TTAATAACA 2940
 GCTTTTTATC CAGTTTGTCA TGGATGTCTT CCATTTATTT GAACATCTCA AAGCTGATGA 3000
 TATGACGGAC ATTGTCAAAA CCATTCATGC TATTCAATCC TTCGATGAAT TGGTTTCTTA 3060
 15 TATCAAGGAA ACTCTGATCA GCTTTTTCGG TCAATACCGT ATGAATGAAA ATGTGGTCAG 3120
 TGTGCTGGAA GTCATTGGTC GTGATTACCA AAAAGAGCTT TCCCTCAAGG ATATCAGTAA 3180
 GGCCCTCTTT ATCAATCCTG TCTATCTAGG GCAGTTGATT AAGCGTGAAA CCGATTGAC 3240
 CTTTGCAGAG TTAATAACA AACAACTAT TAAGGCTGCC CAACAACCTT TGCTTTCAAC 3300
 20 TAGTGACAGC ATCGAAAATA TTTGTTATGC TGTGGTTAC AGTAACCTTG GATATTTCTA 3360
 TAAAGTTTTC CGAAAATTGT GCGGAAAATC GCCAAAAGCC TACCGAAAAC AGGTAGAAAC 3420
 TATACTATAA GATTTGTATT CCTTTACAAA ATG 3453

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 560 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

40 Met Lys Ser Ser Met Lys Asn Trp Arg Gln Asn Arg Met Lys His Phe
 1 5 10 15
 Trp Leu His Thr Leu Leu Arg Thr Tyr Ser Ser Val Met Ile Ile Ile
 20 25 30
 45 Ile Ala Ser Phe Ala Ile Leu Leu Ser Tyr Ala Asp Trp Asp Ser Arg
 35 40 45
 Glu Lys Glu Ala Gln Arg Val Ala Gln Arg Val Thr Ala Arg Thr Val
 50 55 60
 50 Ser Glu Ile Glu Tyr Tyr His Arg Glu Ser Thr Gln Ile Ala Gln Ala
 65 70 75 80
 Leu Val Glu Asn Gln Ala Arg Ile Glu Gly Ile Tyr Lys Tyr Phe Ser

				85					90				95			
	Leu	Ser	Met	Pro	Asp	Tyr	Phe	Tyr	Trp	Gln	Leu	Glu	Arg	Lys	Ala	Ser
5				100					105				110			
	Pro	Tyr	Ile	Ser	Val	Ser	Leu	Tyr	Glu	Asn	Val	Asp	Asp	Leu	Tyr	Val
			115					120				125				
10	Arg	Asn	Asp	Phe	Val	Thr	Gly	Val	Ala	Ile	Ala	Phe	Gln	Asp	Tyr	Lys
		130					135					140				
	Glu	Val	Tyr	Val	Ser	Thr	Lys	Asp	Lys	Arg	Ser	Gly	Glu	Lys	Ile	Arg
	145					150				155					160	
15	Ala	Glu	Asp	Phe	Lys	Pro	Ala	Gly	Asn	Ser	Phe	Ala	Ile	Pro	Val	Ser
				165					170				175			
	Asp	Pro	Val	Ser	Asp	Gln	Asp	Leu	Gly	Val	Ile	Tyr	Ile	Ser	Leu	Asp
			180					185					190			
20	Pro	Ala	Val	Leu	Tyr	His	Ala	Ile	Asp	Asn	Thr	Arg	Gly	His	Thr	Pro
		195						200				205				
	Met	Ala	Val	Thr	Val	Thr	Glu	Pro	Phe	Asp	Thr	Glu	Ile	Phe	His	Ile
		210					215					220				
25	Gly	Glu	Thr	Val	Asp	Lys	Glu	Ser	Glu	Asn	Trp	Leu	Val	Gly	Leu	Thr
	225				230				235					240		
	Ser	His	Gly	Tyr	Gln	Val	Gln	Val	Ala	Val	Pro	Lys	Asn	Phe	Val	Leu
				245					250				255			
30	Gln	Gly	Thr	Val	Thr	Ser	Ser	Ala	Leu	Ile	Val	Gly	Leu	Ser	Leu	Leu
			260					265					270			
	Phe	Ile	Val	Ile	Leu	Tyr	Leu	Thr	Leu	Arg	Gln	Thr	Phe	Ala	Asn	Tyr
		275					280					285				
35	Gln	Lys	Gln	Val	Val	Asp	Leu	Val	Asp	Ser	Ile	Gln	Ala	Ile	Ala	Gln
		290					295					300				
	Gly	Gln	Glu	Gly	Leu	Arg	Ile	Asp	Thr	Leu	Glu	Lys	Asp	Gln	Glu	Leu
	305				310				315					320		
40	Leu	Leu	Ile	Ala	Glu	Thr	Thr	Asn	Asp	Met	Leu	Asp	Arg	Leu	Glu	Lys
				325					330				335			
	Asn	Ile	His	Asp	Ile	Tyr	Gln	Leu	Glu	Leu	Ser	Gln	Lys	Asp	Ala	Asn
			340					345					350			
45	Met	Arg	Ala	Leu	Gln	Ala	Gln	Ile	Asn	Pro	His	Phe	Met	Tyr	Asn	Thr
		355					360					365				
	Leu	Glu	Phe	Leu	Arg	Met	Tyr	Ala	Val	Met	Gln	Ser	Gln	Asp	Glu	Leu
		370					375					380				
50	Ala	Asp	Ile	Ile	Tyr	Glu	Phe	Ser	Ser	Leu	Leu	Arg	Asn	Asn	Ile	Ser
	385				390				395					400		
	Asp	Glu	Arg	Glu	Thr	Leu	Leu	Lys	Gln	Glu	Leu	Glu	Phe	Cys	Arg	Lys

405 410 415
 Tyr Ser Tyr Leu Cys Met Val Arg Tyr Pro Lys Ser Ile Ala Tyr Gly
 5 420 425 430
 Phe Lys Ile Asp Pro Glu Leu Glu Asn Met Lys Ile Pro Lys Phe Thr
 435 440 445
 10 Leu Gln Pro Leu Val Glu Asn Tyr Phe Ala His Gly Val Asp His Arg
 450 455 460
 Arg Thr Asp Asn Val Ile Ser Ile Lys Ala Leu Lys Gln Asp Gly Phe
 465 470 475 480
 15 Val Glu Ile Leu Val Val Asp Asn Gly Arg Gly Met Ser Ala Glu Lys
 485 490 495
 Leu Ala Asn Ile Arg Glu Lys Leu Ser Gln Arg Tyr Phe Glu His Gln
 500 505 510
 20 Ala Ser Tyr Ser Asp Gln Arg Gln Ser Ile Gly Ile Val Asn Val His
 515 520 525
 Glu Arg Phe Val Leu Tyr Phe Gly Asp Arg Tyr Ala Ile Thr Ile Glu
 530 535 540
 25 Ser Ala Glu Gln Ala Gly Val Gln Tyr Arg Ile Thr Ile Gln Asp Glu
 545 550 555 560

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATGAAATCAT CCATGAAAAA TTGG

24

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

5 CTCATCTTGA ATTGTAATAC GATA

24

10 Claims

1. An isolated polynucleotide comprising a polynucleotide sequence selected from the group consisting of:

15 (a) a polynucleotide having at least a 70% identity to a polynucleotide encoding a polypeptide comprising the amino acid sequence of SEQ ID NO:2;

(b) a polynucleotide having at least a 70% identity to a polynucleotide encoding the same mature polypeptide expressed by the histidine kinase gene contained in the *Streptococcus pneumoniae* of the deposited strain;

(c) a polynucleotide encoding a polypeptide comprising an amino acid sequence which is at least 70% identical to the amino acid sequence of SEQ ID NO:2;

20 (d) a polynucleotide which is complementary to the polynucleotide of (a), (b) or (c); and

(e) a polynucleotide comprising at least 15 sequential bases of the polynucleotide of (a), (b) or (c).

2. The polynucleotide of Claim 1 wherein the polynucleotide is DNA.

25 3. The polynucleotide of Claim 1 wherein the polynucleotide is RNA.

4. The polynucleotide of Claim 2 comprising the nucleic acid sequence set forth in SEQ ID NO:1.

30 5. The polynucleotide of Claim 2 comprising nucleotide 450 to 2129 set forth in SEQ ID NO:1.

6. The polynucleotide of Claim 2 which encodes a polypeptide comprising the amino acid sequence of SEQ ID NO:2.

7. A vector comprising the polynucleotide of Claim 1.

35 8. A host cell comprising the vector of Claim 7.

9. A process for producing a polypeptide comprising: expressing from the host cell of Claim 8 a polypeptide encoded by said DNA.

40 10. A process for producing a histidine kinase polypeptide or fragment comprising culturing a host of claim 8 under conditions sufficient for the production of said polypeptide or fragment.

11. A polypeptide comprising an amino acid sequence which is at least 70% identical to the amino acid sequence of SEQ ID NO:2.

45 12. A polypeptide comprising an amino acid sequence as set forth in SEQ ID NO:2.

13. An antibody against the polypeptide of claim 11.

50 14. An antagonist which inhibits the activity or expression of the polypeptide of claim 11.

15. A method for the treatment of an individual in need of histidine kinase polypeptide comprising: administering to the individual a therapeutically effective amount of the polypeptide of claim 11.

55 16. A method for the treatment of an individual having need to inhibit histidine kinase polypeptide comprising: administering to the individual a therapeutically effective amount of the antagonist of Claim 14.

17. A process for diagnosing a disease related to expression or activity of the polypeptide of claim 11 in an individual

comprising:

- (a) determining a nucleic acid sequence encoding said polypeptide, and/or
- (b) analyzing for the presence or amount of said polypeptide in a sample derived from the individual.

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18. A method for identifying compounds which interact with and inhibit or activate an activity of the polypeptide of claim 11 comprising:

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contacting a composition comprising the polypeptide with the compound to be screened under conditions to permit interaction between the compound and the polypeptide to assess the interaction of a compound, such interaction being associated with a second component capable of providing a detectable signal in response to the interaction of the polypeptide with the compound;

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and determining whether the compound interacts with and activates or inhibits an activity of the polypeptide by detecting the presence or absence of a signal generated from the interaction of the compound with the polypeptide.

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19. A method for inducing an immunological response in a mammal which comprises inoculating the mammal with histidine kinase polypeptide of claim 11, or a fragment or variant thereof, adequate to produce antibody and/or T cell immune response to protect said animal from disease.

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20. A method of inducing immunological response in a mammal which comprises delivering a nucleic acid vector to direct expression of histidine kinase polypeptide of claim 11, or fragment or a variant thereof, for expressing said histidine kinase polypeptide, or a fragment or a variant thereof *in vivo* in order to induce an immunological response to produce antibody and/ or T cell immune response to protect said animal from disease.

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